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December 27, 2002, 19:34:03; Search time 253 Seconds (without alignments) 9168.214 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqn_embl.NR1994_DAT:
| SIDS2/gcgdata/geneseq/geneseqn_embl.NR1994_DAT:
| SIDS2/gcgdata/geneseq/geneseqn_embl.NR1995_DAT:
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| SIDS2/gcgdata/geneseqn_embl.NR1999_DAT:
| SIDS2/gcgdata/geneseqn_embl.NR1099_DAT:
| SIDS2/gcgdata/geneseqn_embl.NR2001A_DAT:
| SIDS2/gcgdata/geneseqn_embl.NR2001A_DAT:
| SIDS2/gcgdata/geneseqn_embl.NR2001A_DAT:
| SIDS2/gcgdata/geneseqn_embl.NR2001A_DAT:
| SIDS2/gcgdata/geneseqn_embl.NR2001A_DAT:
| SIDS2/gcgdata/geneseqn_embl.NR2001B_DAT:
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/SIDSZ/gggdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SIDSZ/gggdata/geneseq/geneseqn-embl/NA1984.DAT:*
/SIDSZ/gggdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDSZ/gggdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDSZ/gggdata/geneseq/geneseqn-embl/NA1986.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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1: /SIDS2/gcgdata/g
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Maximum DB seq length: 200000000
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1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	•	Description		Alfalfa plastocyan	. Human KARP-1 DNA.	Cotton promoter re	Senescence-like pr	Pinus radiata prom	Rice anther-specif	O-methyl transfera	Eucalyptus grandis	Arabidopsis BONSAI
		ΩI		AAD38882	AAF31861	AAV40621	AAC62796	ABK17061	AAS15016	AAC62810	ABK17075	ABA91255
		DB		24	22	19	21	24	24	21	24	24
•		Query re Match Length DB I		3548	6078	2614	1038	1038	598	2096	2096	2611
	ф	Query Match		4.4	4.1	4.0	3.9	3.9	3.9	3.9	3.9	3.9
		Score		45	42.4	41	40.6	40.6	40.4	40.4	40.4	40.4
		ult No.	-	~	7	٣	4	S	9	7	æ	σ
		Result No.	i	ပ								O

Flower specific pr Eucalyptus grandis 5' region of human Upstream sequence Hyaluromate syntha Seed-preferred pro PART-1 promoter re Rat glyceraldehyde Rat glyceraldehyde G. max SBP2 DNA 5' Alfalfa AP2 adapto Isoflavone reducta Eucalyptus grandis MIF homologue codit		LIGNMENTS  fragment. recombinant polypeptide; gene cloning;	Bilodeau P; expression regulatory sequence for des and/or RNA, comprises producing lify sequences upstream or downstream
AAC62780 AAX35652 AAX35652 AAAX5034 AAX0328 AAX63331 AAC63331 AAC63331 AAC63331 AAC6263 AAX72244 AAX72244	ABK17081 ABK17081 AAV6859 AAC62809 AAC62809 AAC62779 AAC62802 ABK17067 AAT72245 AAT7667 AAT7667 AAT767668 AAT766768 AAT766768 AAT7668306 AAT766	- ·	i F, Bil an expre
221 221 221 221 221 221 221 221	420102222222222222222222222222222222222	S ~ n·	1532. 214P. Arcand izing polype that
	2815 2867 2867 2867 3111 3111 516 627 627 627 628 648 648 648 648	DNA; t ent in ge in ge cory s	D1: 2001WO-CA01532. D2: 2000US-244214P. EDICAGO INC. D'aoust M, Arcancat71503/50. and characterizing grecombinant polypectide primers that
		standard; 102 (firs) 11astocyan nn regulat plastocyas sativa. 86-A2.	; 2001W ; 2000U ICAGO I D'acust 71503/5
44 wwwwwwww 00 qqqqqqqqq	224 225 226 226 226 236 236 236 236 236 236 236	RESULT 1 AAD38882, ctal XX AC AAD38882; XX	10-MAY-2002. 31-OCT-2001; 2001WO-CA0. 31-OCT-2000; 2000US-244; (MEDI-) MEDICAGO INC. Vezina L, D'aoust M, WPI; 2002-471503/50. Isolating and character expressing recombinant oligonucleotide primers
	0 00 000000	RESSI AAD: XX XX XX XX XX XX XX XX XX XX XX XX XX	XX XX XX X
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expression requiatory sequence for the expression of recombinant polypeptides and/or RNA. The method comprising producing at least one polypeptides and/or RNA. The method comprising producing at least one oligonuclectide primer allows amplification of genomic sequences upstream of the CDNAs. The method is useful for isolating, characterising and identifying a large number of known and unknown promoters that are active under any desired environmental condition to which a cell may be exposed and not just to the exemplified isolation of promoters that are capable of expression in specific conditions. The methods are also useful for cloning genes from any host, or from a specific tissue with such host, from which a cDNA library may be constructed; for the identification and isolation of analogous promoters, signal peptides and structural genes in several species of multicellular and unicellular organisms and as a high throughput identification system of candidate therapeutic targets. The promoter sequence is alfalfat plastocyanin gene coding fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; KARP-1; Ku86 autoantigen related protein; cancer;
immune deficiency disorder; biliary tract cancer; leucine zipper protein;
cytostatic; immunosuppressant; gene therapy; KARP-1 inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is given in a specification relating to an isolated Ku86 Autoantigen Related Protein (KARP-1) nucleic acid molecule. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding leucine zipper protein, KARP-1 for treating cancer and immune deficiency disorder
                                                                    The invention relates to a method for isolating and characterising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3548 BP; 1112 A; 576 C; 727 G; 1133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB Pred. No. 0.00 0; Mismatches
                                   Example 2; Page 68-69; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 51-56; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF31861 standard; DNA; 6078 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                              4.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYBR-) UNIV BROWN RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0173914.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-146208/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human KARP-1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB66590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hendrickson EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6171857-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF31861;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
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RARP-1 nucleic acid and KARP-1 protein are useful for the treatment and/or diagnosis of diseases such as cancer and immune deficiency disorders. They are useful in combination with a KARP-1 inhibitor that inhibits double stranded DNA base repair. Inhibitors of KARP-1 are useful in the diagnosis or treatment of conditions characterised by the loss of KARP-1 activity and in the treatment of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transformation by linking it to a gene of interest, thus enabling the modification of transgenic cotton fibre cells.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents an expansin promoter region from Gossypium hirsutum. This has been sequenced and found to be approximately 2200 bp in length, and is immediately 5' to the cotton fibre expansin coding region. The promoter can be used in cotton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA containing the promoter of the cotton expansin gene - use for tissue-selective expression of genes that alter cotton fibre
                                                                                                                                                                                       .;
0
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0
                                                                                                                                                        Length 6078;
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                                                                                                                          Sequence 6078 BP; 1806 A; 1301 C; 1392 G; 1543 T; 36 other;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2614 BP; 892 A; 436 C; 401 G; 882 T; 3 other;
                                                                                                                                                                                                                    44
                                                                                                                                                                                                                                  9 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGAA 52
                                                                                                                                                       Score 42.4; DB 22;
Pred. No. 0.028;
0; Mismatches 1;
                                                                                                                                                                                                                 1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAT 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0%; Score 41; DB 19;
100.0%; Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                     Cotton promoter region from an expansin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig la-d; 26pp; English.
                                                                                                                                                                                                                                                                                                                           AAV40621 standard; DNA; 2614 BP
                                                                                                                                                       ch 4.1%;
1 Similarity 97.7%;
43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0034914.
                                                                                          e.g. biliary tract cancer.
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CALJ ) CALGENE INC.
                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stalker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9830698-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                      26-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phenotype
                                                                                                                                                                                                                                                                                                                                                        AAV40621;
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Matches
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Gaps

ó 54

5; Indels

; DB 24; Length 3548; 0.0029;

5

RESULT 4

AAC62796

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The invention relates to isolated promoter sequences from Pinus radiata and Bucalyptus grandis, comprising a sequence chosen from leaf., root., flower., pollen., bud., meristem-specific promoters or temporally regulated promoters such as xylogenesis-specific promoters. The promoter polypeptides and their related polynucleotides are useful in the production of genetic constructs, used for modifying gene expression in a target organism, in particular a plant. The method is useful for modifying expression of a polynucleotide that comprises an intron sequence, through removal of the intron sequence. The method is useful correction sequence are useful in development of plants, and cellular responses to external stimulus, such as environmental factors and disease pathogens. The sequences are useful in genome and physical mapping, in positional cloning of genes, in various assays to determine biological activity, to carse antibodies, to isolate corresponding interacting proteins and other compounds, and to quantitatively determine levels of interacting proteins of or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata
                                                                                                                                                                                                                                                                                                                      Novel polynucleotide promoter sequences from Pine and Eucalyptus useful for modifying expression of endogenous and/or heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAAA----TGAGAACATGATAAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40.6; DB 24; Length 1038;
Pred. No. 0.037;
0; Mismatches 24; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice; promoter; gene therapy; transcription; monocot; anther; chromosome mapping; gene mapping; antisense technology; plant genetic engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1038 BP; 298 A; 220 C; 233 G; 287 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ATGCATATACTGCTGAGAGATAACATCACAATTCACA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 CIGIGIAAATICATGCTAGICACCATAACITITICICA 96
                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS IND LTD.
                                                                                                                                                                                                                 Eagleton C, Lasham A;
                                                                                                                                                                                                                                                                                                                                                 for modifying expression of endogenou polynucleotides in transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 73-74; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice anther-specific promoter #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.9%; 71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS15016 standard; cDNA; 598
                                        20-JUN-2001; 2001WO-NZ00115.
                                                                                     2000US-0598401
                                                                                                       2000US-0724624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match ,
Best Local Similarity 71.19
Watches 69; Conservative
                                                                                                                                                                                                                                                         WPI; 2002-114583/15
                                                                                                                                                                                                                   Perera R, Rice S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
                                                                                                                                                                                                                                                                                    P-PSDB; AAU80754
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                                                                                     20-JUN-2000;
                                                                                                       28-NOV-2000;
27-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to promoter sequences from eucalyptus and pine. The present sequence is one such promoter. This sequence is useful for modulating the transcription of DNA sequences of interest. The sequences may also be used to tag or identify an organism or its reproductive material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis; temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel promoter sequences useful for modulating transcription of plant DNA sequences of interest and production of polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ITACTATAGGGCACGCGTGGTCGACGCCCGGGCTGGTATGAAGGTGGGAACCTCACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40.6; DB 21; Length 1038;
Pred. No. 0.037;
0; Mismatches 24; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1038 BP; 298 A; 220 C; 233 G; 287 T; 0 other;
                                                                                                                                  Senescence-like protein promoter coding sequence #1.
                                                                                                                                                                          Promoter; eucalyptus; pine; gene transcription; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ATGCATATACTGCTGAGAGATAACATCACAATTCACA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 crgranarrcargcragrcaccaraacrrrcrca 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinus radiata promoter polynucleotide #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Pages 57-58; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eagleton CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР
    AAC62796 standard; DNA; 1038 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK17061 standard; cDNA; 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.9%;
Best Local Similarity 71.1%;
Matches 69; Conservative (
                                                                                                                                                                                                                                                                                                                                                   24-FEB-2000; 2000WO-NZ00018
                                                                                                                                                                                                                                                                                                                                                                                           99US-0276599
99US-0146591
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                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perera R, Rice SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-647236/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB28136
                                                                                                                                                                                                                                                              WO200058474-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinus radiata
                                                                                                                                                                                                                     Pinus radiata.
                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1999;
30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                        05-OCT-2000
                                                                                       02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK17061;
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ABK1706 RESULT

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and pine. The present sequence is one such promoter. This sequence is useful for modulating the transcription of DNA sequences of interest. The sequences may also be used to tag or identify an organism or its reproductive material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated promoter sequences from Pinus radiata and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-, flower. , pollen-, bud-, meristem-specific promoters or temporally regulated promoters such as xylogenesis-specific promoters. The promoter polypeptides and their related polynucleotides are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide promoter sequences from Pine and Eucalyptus useful for modifying expression of endogenous and/or heterologous polynucleotides in transgenic plants \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis; temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
                                                                                                                              Novel promoter sequences useful for modulating transcription of plant DNA sequences of interest and production of polypeptides
                                                                                                                                                                                                                      promoter sequences from eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                    21; Length 2096;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                  Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucalyptus grandis promoter polynucleotide #31.
                                                                                                                                                                                                                                                                                                                                                                    Score 40.4; DB 2
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LID.
(FLET-) FLETCHER CHALLENGE FORESTS IND LID.
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lasham A;
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                    Claim 1; Pages 61-62; 93pp; English.
                                      Eagleton CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 78; 121pp; English.
                                                                                                                                                                                                                        The present invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK17075 standard; cDNA; 2096 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eagleton C,
                                                                                                                                                                                                                                                                                                                                                                   3.9%;
ilarity 97.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2001; 2001WO-NZ00115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2000; 2000US-0598401
28-NOV-2000; 2000US-0724624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-114583/15.
P-PSDB; AAU80760.
                                                                       WPI; 2000-647236/62
P-PSDB; AAB28142.
                                      Rice SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perera R, Rice S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200198485-A1.
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Local S. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer
                                      Perera R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK17075;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        encode promoter components of the cellular activation and transcription the paparatus (5' cis regulatory DNA sequences). The sequences may be used in the modification of gene activation and/or expression in eukaryotes, especially rice and other monocots. They have many applications in polymerase chain reaction (PCR) technology, for the study of gene mapping, in polymerase chain reaction (PCR) technology, for the study of gene function and expression in vivo, specific down-regulation of target genes, and in the production of sense and/or antisense nucleic acids. The present sequence represents rice anther-specific promoter #2 as described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to plant polynucleotide sequences from rice which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTGGAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice promoter sequences (I) useful in plant genetic engineering and molecular biology studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40.4; DB 24; Length 598; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.031;
hes 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 598 BP; 174 A; 131 C; 113 G; 179 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Promoter; eucalyptus; pine; gene transcription; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O-methyl transferase promoter coding sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC62810 standard; DNA; 2096 BP.
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1B; 47pp; English.
                                                                       2000US-199870P.
2000US-217891P.
2000US-218366P.
2000US-277231P.
2000US-237736P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2000; 2000WO-NZ00018.
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99US-0146591
                                      26-APR-2001; 2001WO-US13544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                            Perera JR, Lu M, Ray A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Conservative
                                                                                                                                                                                                         (AKKA-) AKKADIX CORP.
                                                                                                                                                                                                                                                                              WPI; 2002-041419/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200058474-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 GCATAT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TAATAT 66
                                                                                                           13-JUL-2000;
23-AUG-2000;
03-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999;
30-JUL-1999;
                                                                                              12-JUL-2000;
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                                                                          26-APR-2000;
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Query Match

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AAC62810 RESULT

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isolated BON1, BON2, BON3, BAP1 and BAL nucleic acids (see

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                                                                                                external stimulus, such as environmental factors and disease pathogens. The sequences are useful in genome and physical mapping, in positional cloning of genes, in various assays to determine biological activity, to raise antibodies, to isolate corresponding interacting proteins and other compounds, and to quantitatively determine levels of interacting proteins or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata and Eucalyptus grandis polynucleotides and PCR primers used in the method
                  target organism, in particular a plant. The method is useful for modifying expression of a polynucleotide that comprises an intron sequence, through removal of the intron sequence. The method is useful for modifying growth and development of plants, and cellular responses to
  expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New phospholipid binding proteins and nucleic acids, useful for modulating plant growth homeostasis, controlling cell expansion and cell division, or producing plants where larger fruits and increased biomass are desired
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thallana. The coding region of the BONI gene is given in ABA91256. The BONI gene permits wild-type Arabidopsis plants to maintain a relatively constant size over a wide range of temperatures. Thus, bonl null mutants produce miniature fertile plants at 22 degrees C, but a wild-type phenotype at 28 degrees C. BONI has a direct role in regulating cell expansion and cell adivision at temperatures lower than those at which Arabidopsis is normally grown. The BONI protein (see AAM50644) contains a Caz+-dependent phospholipid binding domain and is associated with the plasma membrane. BONI belongs to the copine gene family, which is conserved from protozoa to humans. The invention is directed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BONSAII; BONI; phospholipid binding protein; growth; homeostasis; thermotolerance; transgenic plant; plant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis BONSAII (BON1) gene, involved in growth homeostasis.
                                                                                                                                                                                                                                                                                                                                                                    .
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Pred. No. 0.065;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of the BONSAII (BON1) gene of
        dene
                                                                                                                                                                                                                                                                                  Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 other;
  genetic constructs, used for modifying
                                                                                                                                                                                                                                                                                                                                                                                                           2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                3 TTACTATAGGGCACGCGTGGTCGACGCCCGGCTGGTCTGA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 8A; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA91255 standard; DNA; 2611 BP
                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                            3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-2001; 2001WO-US20172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-2000; 2000US-213863P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grisafi P, Fink GR;
                                                                                                                                                                                                                                                                                                                                                 97.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-139899/18.
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                              of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200697-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA91255;
                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to promoter sequences from eucalyptus and pine. The present sequence is one such promoter. This sequence is useful for modulating the transcription of DNA sequences of interest. sequences may also be used to tag or identify an organism or its reproductive material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel promoter sequences useful for modulating transcription of plant DNA sequences of interest and production of polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                        Gaps
     ABA91256-60), which encode proteins (see AAM50644-48) that are necessary for normal growth, controlling cell expansion and cell division, affecting the size and rate at which the plant grows when exposed to lower temperatures. Transgenic plants are provided that are smaller than the wild-type as a result of inhibition of BON1, BON2, BON3, BAP1 and/or BAL, especially angiosperms and gymnosperms, ornamental plants and turfgrass. Transgenic plants are also provided that are larger than the wild-type as a result of plants and blomass plants. Modulation of these genes provides that are larger than the wild-type as a result of plants and biomass plants. Modulation of these genes provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                        24; Length 2611;
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Pred. No. 0.029;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                          Sequence 2611 BP; 809 A; 429 C; 498 G; 866 T; 9 other;
                                                                                                                                                                                                                                                                                                                                     2603 CTTACTATAGGGCACGCGTGGTCGACGCCCGGGCTGGTCTG 2562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 411 BP; 112 A; 118 C; 80 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Promoter; eucalyptus; pine; gene transcription; ds.
                                                                                                                                                                                                                                                                                                                        1 CTTACTATAGGGCACGCGTGGTCGACGCCCGGGCTGGTATG 42
                                                                                                                                                                                                                                                      Score 40.4; DB 2 Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flower specific promoter coding sequence #2.
                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eagleton CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 53; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        вР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.9%;
                                                                                                                                                                                                                                                          3.98;
97.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000; 2000WO-NZ00018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0276599
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC62780 standard; DNA; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0146591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.3
Matches 42; Conservative
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-647236/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eucalyptus grandis.
                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200058474-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000.
                                                                                                                                                                                             temperature
                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perera R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC62780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                           AAC62780
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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555555555555555888
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4 ACTATAGGGCACGCGTCGACGGCCCGGGCTGGTATGAAGGTG 48

δ

human heparanase CDNA.

(first entry)

g

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Heparanase; hpa; modulator; heparin-binding growth factor; cellular response; cytokine; cell interaction; plasma lipoprotein; cellular susceptibility; infection; disintegration; response; neurodegenerative plaque; wound healing; angiogenesis; restenosis; athersolerosis; inflammation; neurodegenerative disease; neutralise; plasma heparin; micrometastasis; autoimmune lesion; renal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human polynucleotide useful for treating angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FRIE/) FRIEDMAN M M.
(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
(INSI-) INSIGHT STRATEGY & MARKETING LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Page 69; 63pp; English.
                         AAX35652 standard; cDNA; 594 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restenosis, and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feinstein E, Pecker I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-302255/25.
                                                                                                                                                                                                                                                                                                                                                                                                                            W09911798-A1.
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                           5' region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1997;
                                                                                                               09-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1999.
                                                                     AAX35652;
AAX35652
                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated promoter sequences from Phins radiata and Eucalyptus grandis, comprising a sequence chosen from leaf-, root-, flower-, pollen-, bud., meristem-specific promoters or temporally regulated promoters such as xylogenesis specific promoters. The promoter properties and their related polynucleotides are useful in the promoter of genetic constructs, used for modifying gene expression in a target organism, in particular a plant. The method is useful for modifying expression of a polynucleotide that comprises an intron sequence, through removal of the intron sequence. The method is useful for modifying growth and development of plants, and cellular responses to external stimulus, such as environmental factors and disease pathogens. The sequences are useful in genome and physical mapping, in positional cloning of genes, in various assays to determine biological activity, to raise antibodies, to isolate corresponding interacting proteins and toquantitatively determine levels of interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds. Sequences ABK17125 represent Pinus radiata
                                                                                                                                                                                                                                                                                                                 Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis; temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide promoter sequences from Pine and Eucalyptus useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.2; DB 24; Length 411; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for modifying expression of endogenous and/or heterologous
Sequence 411 BP; 112 A; 118 C; 80 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                       Eucalyptus grandis promoter polynucleotide #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FLET-) FLETCHER CHALLENGE FORESTS IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice S, Eagleton C, Lasham A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides in transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 68-69; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                      BP
                                                                                                                                      ABK17045 standard; cDNA; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2001; 2001WO-NZ00115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2000; 2000US-0598401.
28-NOV-2000; 2000US-0724624.
                                                                                                                                                                                                                              (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-114583/15.
                                                                                                                                                                                                                                                                                                                                                                                                         Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200198485-A1.
                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                               PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perera R,
                                                                                                                                                                                  ABK17045;
                                                                                          RESULT 11
                                                                                                                 ABK17045
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Vlodavsky I;

98WO-US17954. 98US-0109386 97US-0922170

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The specification describes a polypeptide having heparanase (hpa) activity. The recombinant protein is used as a modulator of heparin-binding growth factors, cellular responses to heparin-binding growth factors and cytokines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections or disintegration of neurodegenerative plaques. Heparanase may be useful for conditions such as wound healing, anglogenesis, restenosis, athersclerosis, inflammation, neurodegenerative diseases, and viral infections. Mammalian heparanase can be used to neutralize plasma
                                                                                                                                                                                                                                                                                                       immunodetection and diagnosis of micrometastases, autoimmune lesions, and renal failure in biopsy specimens, plasma samples, and body fluids. The present sequence represents the 5' sequence of human heparanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 594;
                                                                                                                                                                                                                                                                             heparin, and anti-heparanase antibodies may be applied for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 594 BP; 133 A; 134 C; 209 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TIACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 20;
Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.9%; Score ... 100.0%; Pred. No. 0.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA75054 standard; cDNA; 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                and renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA75054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA75054
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; 0

Gaps

0;

Indels

3;

0; Mismatches

93.3%;

Conservative

42;

Matches

ŏ qq RESULT 12

15-JAN-2001

08-SEP-2000

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Seed-preferred promoter; maize; end gene; endosperm; end1; end2; fatty acid; starch profile; carbohydrate profile; amino acid content; agronomic; insect resistance; disease resistance; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                promoter for the hyaluronate synthase gene. It was isolated from human cDNA sources. The DNA is useful for screening a drug enhancing or inhibiting production of hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seed-preferred manner, for
                                                                                                                                                                                                                                                                                                                                                                               represents the DNA of the invention, and can act as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a seed-preferred promoter isolated from manendosperm specific genes, endl or end2. The promoter is capable of
                                                                                                                                                                                                                                                                           A promoter for hyaluronate synthase gene - used for screening of modulators of the \ensuremath{\mathsf{enzyme}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.9%; Score 40; DB 20; Length 1680;
100.0%; Pred. No. 0.077;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1680 BP; 452 A; 381 C; 467 G; 380 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linnestad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTACTATAGGGCACGCGTGGTCGACGCCCGGGCTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seed-preferred promoter-2 from maize end gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olsen O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           maize promoter driving transcription in stably transforming plant cells \, -
                                                                                                                                                                                                 ADSK-) ADVANCED SKIN RES KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Pages 35-36; 43pp; English.
                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 5-6; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martino-Catt SJ, Lappegard KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ51547 standard; DNA; 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0098230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US19604
                                                                                                                                                           97JP-0107624.
                                                                                                                97JP-0107624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         grain characteristic; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-256648/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-1998;
  Homo sapiens
                                      JP10295383-A
                                                                                                                                                         24-APR-1997;
                                                                                                                  24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2000.
                                                                            10-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ51547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ51547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an upstream sequence of cDNA encoding encodes a human protein with heparanase catalytic activity. The heparanase (hpa) polynucleotide is useful in gene therapy, particularly in treating tumour, inflammation or autoimmunity. Particularly the polynucleotide is useful in medulating the bioavailability of heparin-binding growth factors, cellular responses to heparin-binding growth factors (e.g. interleukin (IL)-8), cell interaction with plasma of protozoa infections, or disintegration of neurodegenerative plaques. The polynucleotide is also useful in wound healing (e.g. thermal, chemical or radiation burns), and in the treatment of angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-Straussler Syndrome or Creutzfeldt-Jakob disease), and some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding a polypeptide having heparanase activity, useful in wound healing and in gene therapy, particularly in treating tumour, inflammation, autoimmunity, neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                              heparanase; gene therapy; tumour; inflammation; autoimmunity;
                                                                                               heparin-binding growth factor; cytokine; neurodegenerative plaque; wound healing; infection; burn; andjogenesis; restenosis; atherosclerosis; inflammation; neurodegenerative disease; Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.9%; Score 40; DB 21; Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 594 BP; 133 A; 134 C; 209 G; 118 T; 0 other;
                                        Upstream sequence of human cDNA encoding heparanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TTACTATAGGGCACGCGTCGACGACGGCCCGGCTGGTAT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyaluronate synthase; promoter; human; hyaluronic acid production inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                       (INSI-) INSIGHT STRATEGY & MARKETING LTD.
(HADA-) HADASIT MEDICAL RES SERVICES & DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial or protozoa infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feinstein E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Page 127; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hyaluronate synthase promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV08328 standard; cDNA; 1680
                                                                                                                                                                                                                                                                                                                          14-FEB-2000; 2000WO-US03542,
                                                                                                                                                                                                                                                                                                                                                                 99US-0258892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pecker I, Vlodavsky I,
                                                                                                                                                                                                                                                                                                                                                                                                                            (HADA-) HADASIT MEDIC
(FRIE/) FRIEDMAN M M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-579289/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 40; Conserv
                                                                                                                                                                                                                                            WO200052178-A1.
                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1999;
                                                                                                                                                                                                       Homo sapiens
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Query Match

Best Loc Matches

viral,

AAV08328

RESULT 14

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Gaps

; 0

maize

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driving transcription in a seed-preferred manner and can be used in an expression cassette, to stably transform plant cells. The expression consent of seeds, alter can be used to modify the fatty acid content of seeds, alter the starch or carbohydrate profile, and/or alter the amino acid content of the starch or carbohydrate profile, and/or alter the amino acid content of traits for agronomics, including insect resistance, disease resistance, and grain characteristics.

C traits for agronomics, including insect resistance, disease resistance, xx

S Sequence 1224 BP; 378 A; 239 C; 182 G; 425 T; 0 other;

Ouery Match

Best Local Similarity 95.3%; Pred. No. 0.074;

Matches 41; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TACTATAGGGGCACGCGGGCTCGCTATGAAG 45

I TACTATAGGGCACGCGTGGTCGACGCCCGGCTGGTAAAAAG 43
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Search completed: December 27, 2002, 22:42:34 Job time: 256 secs

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Sequence 7, Appli
Sequence 7, Appli
Sequence 11, Appli
Sequence 13, Appl
Sequence 14, Appli
Sequence 5, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 13, Appli
Sequence 15, Appli
Sequence 30, Appli
Sequence 31, Appli
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Sequence 31, Appli
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5849.575 Million cell updates/sec
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                                                                 December 28, 2002, 00:01:58; Search time 54 Seconds
                                                                                                                                                                                                                                                                                                                      1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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US-08-222-463-14

US-09-273-145-11

US-09-377-688-4

US-09-377-688-4

US-09-277-689-13

US-09-276-599-13

US-09-276-599-13

US-09-276-599-13

US-09-276-599-13

US-09-276-599-13

US-09-276-599-13

US-09-545-814-28

US-09-545-814-15

US-09-545-814-4

US-09-545-814-4
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             nucleic search, using sw model
                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                   cttactatagggcacgcgtg.
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Maximum DB seq length: 200000000
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1030
1 cttactataqqqcac
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Match Length
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Perfect score:
Sequence:
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39.8
39.6
39.6
39.39
38.4
38.4
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GENERAL INFORMATION:

APPLICANT: Hendrickson, Eric

APPLICANT: Hendrickson, Eric

TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and

TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity

FILE REFERENCE: B0877/7017/HK

CURRENT APPLICATION NUMBER: US/09/173,914

CURRENT FILING DATE: 1998-10-16

EARLIER APPLICATION NUMBER: 60/064,557

BARLIER FILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1 ö Sequence 1688, Applayequence 53, Appla Sequence 53, Appla Sequence 5, Appla Sequence 6, Appla Sequence 1291, Appla Sequence 21, Appla Sequence 21, Appla Sequence 5, Appla Sequence 20, Appla Sequence 20, Appla Sequence 21, Appla Sequence 21, Appla Sequence 21, Appla Sequence 22, Appla Sequence 22, Appla Sequence 21, Appla Sequence 22, Appla Sequence 21, Appla Sequence 22, Appla Sequence 21, Appla Sequence 21, Appla Sequence 21, Appla Sequence 41, Appla Appla Sequence 41, Appla Appla Sequence 41, Appla Appla Appla Sequence 41, Appla App Gaps Sequence ; 0 ch 4.1%; Score 42.4; DB 4; Length 6078; 1 Similarity 97.7%; Pred. No. 0.0041; 43; Conservative 0; Mismatches 1; Indels 0 52 44 1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAA US-09-134-001C-1688
US-08-134-001C-1688
US-08-178-4948-53
US-08-178-190A-5
US-08-196-300A-5
US-08-196-300A-5
US-08-196-300A-3
US-08-134-001C-1291
US-09-134-01C-1291
US-08-155-587-37
US-08-175-587-37
US-08-175-34A-21
US-08-176-394A-20
US-08-74-394A-21
US-08-74-394A-21
US-08-74-394A-21
US-08-74-394A-21
US-08-74-394A-21
US-08-74-394A-21
US-08-74-394A-21 ALIGNMENTS US-09-173-914-1 ; Sequence 1, Application US/09173914 ; Patent No. 6171857 NAME/KEY: unsure
LOCATION: (610)...(610)
NAME/KEY: unsure
LOCATION: (612)...(610) ...(2175) (1014)...(1014) 5555 1889 1881 3718 3718 3740 3740 3740 3760 500 500 500 3064 246240 246240 246240 6202 LOCATION: (234)...(234) NAME/KEY: unsure LOCATION: (453)...(453) ORGANISM: Homo Sapiens FEATURE: NAME/KEY: unsure LOCATION: (178)...(178) Best Local Similarity Matches 43; Conserv NAME/KEY: unsure LOCATION: (232)...
NAME/KEY: unsure NAME/KEY: unsure LOCATION: (473)... unsure (2175). unsure NAME/KEY: unsure (230)6078 US-09-173-914-1 NAME/KEY: NAME/KEY: COCATION: LOCATION: LOCATION: Query Match TYPE: DNA LENGTH: ð qq 0000

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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 CTCACTATAGGGCACGCGTGGTCGACGCCCCGGCTGGTCTGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
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COMPUTER: IBM PC.Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGA
                                                                        GENERAL INFORMATION:
APPLICANT: Grimes, et al.
TITE OF INVENTION: Sucrose binding proteins
FILE REFERENCE: 4630-50206
CURRENT APPLICATION NUMBER: US/09/424,283
CURRENT FILING DATE: 1990-11-19
PRIOR APPLICATION NUMBER: PCT/US98/10465
PRIOR PPLICATION NUMBER: US 60/047,568
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 6
LENGTH: 3718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FLAKNER, F. G.
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                  3.9%; Score 39.8;
95.3%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY_AGGNT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: Foley & Lardner: 1800 Diagonal Road, Suite 500 Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
       RESULT 2
US-09-424-283-6
; Sequence 6, Application US/09424283
; Patent No. 6437219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 95.3
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Glycine max
US-09-424-283-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: USA
22313-0299
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Batent No. 6462257

GENERAL INFORMATION:
APPLICANT: Pullman, Gerald
APPLICANT: Pertrea, Ranjan
APPLICANT: Pertrea, Ranjan
APPLICANT: PERTREACE: PROMOTER AND
TITLE OF INVENTION: WETHODS OF USING THE SAME
FILE REFERENCE: IPST0009
CURRENT APPLICATION NUMBER: US/09/323,195A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                       681 GGACCTCCCTGCTGCTGCCAACTGCCAACCAGACCTGGCATGGCCTGGTGGCGTCAT 740
                                                                                                                                                                                                                                    561 IGGCACCCGAIGGAIGICCCAICCGAACIIGICICCAACICIGCAITITCGGIICAGAGC 620
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Pred. No. 0.011;
0; Mismatches 5; Indels
                                                                                                                                                        Query Match 3.8%; Score 39.6; DB 1; Length 7 Best Local Similarity 5.0%; Pred. No. 0.035; Matches 15; Conservative 163; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Grimes, et al.
TITLE OF INVENTION: Sucrose binding proteins
FILE REFERENCE: 4630-50206
CURRENT APPLICATION NUMBER: US/09/424,283
CURRENT FILING DATE: 1999-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/09424283; Patent No. 6437219; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.8%;
7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.0
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Best Local Similarity 89.4
Matches 42; Conservative
                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                      US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pinus taeda
                                                       TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-323-195A-1
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LENGTH: 341
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Length 2791;

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3.7%;
ilarity 87.5%;
Conservative
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US-09-276-599-14
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Best Local Similarity
Matches 38; Conserv
                        Query Match
Best Local Similarity
Matches 42; Conserv
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LENGTH: 763
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TITLE OF INVENTION: Methods and Compositions for Immunomodulation
FILE REFERENCE: 9579-21
CURRENT APPLICATION UNBER: US/09/570,367C
CURRENT FILING DATE: 2000-05-05
PRIOR FULING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2791
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                                                                                                                                                                                                                            Query Match 3.8%; Score 39; DB 4; Length 4526; Best Local Similarity 100.0%; Pred. No. 0.042; Matches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                          2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTA 40
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09377648

Patent No. 6225529
GENERAL INFORMATION:
APPLICANT: Lappegard, Kathryn
APLICANT: Martino-Catt, Susan
TITLE OF INVENTION: Seed-Preferred Promoters
FILE REFERENCE: 0869
CURRENT APPLICATION NUMBER: US/09/377,648
CURRENT FILING DATE: 1999-08-19
CURRENT FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FRALESEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38.4; DB 4
Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US98/10465
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: US 60/047,568
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 7
LENGTH: 4526
         PCT/US98/10465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09570367C; Patent No. 6338851; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.7%;
ilarity 97.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
COGGANISM: MUS musculus
US-09-570-367C-1
                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Glycine max
US-09-424-283-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1)...(922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: promoter; LOCATION: (1)...(95
US-09-377-648-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Zea mays
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                                         Indels
                                                                                                    1 ACTATAGGGCACGCGTGGTCGACGCCCGGGCTGGTACTGAGAAA 48
                                                                                  4 ACTATAGGGCACGCGTGGTCGACGCCCCGGGCTGGTATGAAGGTGGGA 51
                                                                                                                                                                                                                 Sequence 13, Application US/09276599; Patent No. 6380459; GENERAL INFORMATION:

APPLICANT: Perear, J. Ranjan
APPLICANT: Perear, J. Ranjan
APPLICANT: Perear, J. Ranjan
TITLE OF INVENTION: Composition and methods for the
TITLE OF INVENTION: modification of gene expression
FILE REFERENCE: 11000.1306
CURRENT APPLICATION UNBERS: US/09/276,599
CURRENT FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Percent, J. Ranjan
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Composition and methods for the
TITLE OF INVENTION: modification of gene expression
FILE REFERENCE: 11000.1036
CURRENT APPLICATION NUMBER: US/09/276,599
CURRENT FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASELSEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 3.7%; Score 38; DB 4; Le Best Local Similarity 100.0%; Pred. No. 0.034; Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 4; Le
Pred. No. 0.022;
Score 38.4; DB 4;
Pred. No. 0.051;
0; Mismatches 6;
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; Sequence 5, Application US/09323195A
; Patent No. 646257
; GENERAL INFORMATION:
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; Sequence 14, Application US/09276599
; Patent No. 6380459
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3.6%; Score 37.4; DB 4; Length 48; 97.4%; Pred. No. 0.012; tive 0; Mismatches 1; Indels
                                                                                                                 APPLICANT: Nishi, Kazunori
APPLICANT: Hikichi, Yukiko
APPLICANT: Shinteni, Yasushi
TITLE OF INVENTION: NOVEL FAS LIGAND-LIKE PROTEIN, ITS
TITLE OF INVENTION: PRODUCTION AND USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       ADDRESSEE: David G. Conlin, Esq.
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & USHMAN, ILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGT 39
                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/02480
FILING DATE: July 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: David G. Conlin
REGISTRATION NUMBER: 27, 026
REFERENCE/DOCKET NUMBER: 342/47694
TELECOMMUNICATION INFORMATION:
TELEPHONE: 611-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/913,014A
FILING DATE: 04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18:
                                                                                                                                                                                                                                                                     STREET: 130 Water Street CITY: Boston,
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 97.4 Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single
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MEDIUM TYPE: Diskett
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CORGANISM: Mus musculus
US-09-570-367C-1
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                                                                                                                                                                                                                                                                                                                        USA
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US-09-570-367C-1/C
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LENGTH: 2791
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Pred. No. 0.033;
0; Mismatches 2; Indels
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0.065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAA 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.8; DB 4;
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09424283
Patent No. 6437219
GENERAL INFORMATION:
APPLICANT: Grimes, et al.
TILLE OF INVENTION: Sucrose binding proteins
FILE REFERENCE: 4630-56206
CURRENT APPLICATION NUMBER: US/09/424,283
CURRENT FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: PCT/US98/10465
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1998-05-21
PRIOR PLING DATE: 1998-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
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Patent No. 6235878
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is a,
is a,
is a,
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OTHER INFORMATION: n at 489 is
OTHER INFORMATION: n at 504 is
OTHER INFORMATION: n at 522 is
OTHER INFORMATION: n at 522 is
OTHER INFORMATION: n at 533 is
OTHER INFORMATION: n at 543 is
OTHER INFORMATION: n at 549 is
US-09-323-195A-5
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Best Local Similarity 95.18
Matches 39; Conservative
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Best Local Similarity 95.19
Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: CDS
; LOCATION: (119)...(1588)
US-09-424-283-5
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pinus taeda
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US-09-424-283-5/c
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US-08-913-014A-18
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LENGTH: 1924
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GENERAL INFORMATION:

BAPLICANT: GARCASYNSKI, Reginald M.

TITLE OF INVENTION: Methods and Compositions for Immunomodulation
FILE REFERENCE: 9579-21
CURRENT APPLICATION NUMBER: US/09/570,367C
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/064,764
PRIOR FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
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10 CTCACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGT 48
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LENGTH: 1478
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Sequence No. 6416977

GENERAL INFORMATION:

APPLICANT: BECHCY, Anna M.

TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION. USES THEREOF

FILE REFERENCE: FC-5-C1

CURRENT APPLICATION NUMBER: US/09/545,814

CURRENT FILING DATE: 1999-04-09

PRIOR PILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATCHIN VOE: 2.1

SEQ ID NO 30
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Patent No. 6416977

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FILLS OF INVENTION:
FILE 
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                                        Indels
                                                                                                       1;
       Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Tagged Ctenocephalides felis
       Rest Local Similarity 97.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1)..(1467)
US-09-545-814-28
                                                                                                                                                                                                                                                                                                                                 US-09-545-814-28/c
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LENGTH: 1478
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US-09-545-814-30
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                                                                                              Gaps
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                                                     Length 1478;
                                                                                              Indels
                                                                                            0; Mismatches 128;
                                                       Score 37.2; DB 4;
Pred. No. 0.087;
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, ORGANISM: Tagged Ctenocephalides felis
US-09-545-814-30
                                                       Query Match 3.6%;
Best Local Similarity 47.1%;
Matches 114; Conservative
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December 27, 2002, 23:38:28 ; Search time 252 Seconds (without alignments) 9204.596 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
| SIDS2/gcgdata/geneseq-geneseqn-embl/NA1986.DAT:*
| SIDS2/gcgdata/geneseq-geneseqn-embl/NA1989.DAT:*
| SIDS2/gcgdata/geneseq-geneseqn-embl/NA1989.DAT:*
| SIDS2/gcgdata/geneseq-geneseqn-embl/NA1999.DAT:*
| SIDS2/gcgdata/geneseq-geneseqn-embl/NA1991.DAT:*
| SIDS2/gcgdata/geneseq-geneseqn-embl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cttactatagggcacgcgtg......tgtatatatacaaggtctgg 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4370478
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                OM nucleic
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Perfect sc
Sequence:
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                                                                                                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Alfalfa plastocyan	Human KARP-1 DNA.	Cotton promoter re	Senescence-like pr	Pinus radiata prom	Rice anther-specif	O-methyl transfera	Eucalyptus grandis	Arabidopsis BONSAI
		Π	AAD38882	AAF31861	AAV40621	AAC62796	ABK17061	AAS15016	AAC62810	ABK17075	ABA91255
		80	24	22	13	21	24	24	21	24	24
		Match Length DB	3548	6078	2614	1038	1038	598	2096	2096	2611
æ	Query	Match 1	4.4	4.1	4.0	3.9	3.9	3.9	3.9	3.9	3.9
		Score	45	42.4	41	40.6	40.6	40.4	40.4	40.4	40.4
	1t	No.	: : ~	7	٣	4	2	9	7	80	6
	Result	z	; 0								ပ

	1948 T. thermophila dell 1948 T. thermophila dell 2859 Flower specific pr Flower specific pr Eucalptus grandis Rice tubulin-like Flower specific pr Eucalptus grandis Rice tubulin-like Flower specific pr Eucalptus grandis Alfalfa plastocyan Pollen specific pr P	PrFil G. ma. Asperir Maize Maize Glyce Eucal: Isofli Eucal:	ALIGNMENTS . g fragment.	recombinant polypeptide, gene cloning;	Bilodeau P; expression regulatory sequence for
21 AAC62780 24 ABK17045 20 AAX35652 20 AAX35654 20 AAX08328 21 AAZ51547 24 ABL50287 24 AAD38881 24 ABK17053 25 AAC62816			AL 548 BP.	ence;	
411 411 594 594 1680 1224 2385 2475 2565 3716 3775 288 288	515 2492 2867 311 311 516 927 940 1126	1242 4526 1196 5031 382 382 382 648 648	NA; entr gen	y s n; CA0 244	D'aoust M, Arcand F. 471503/50. and characterizing an recombinant polypept.
			82 standard; D 82; -2002 (first	re las ati 5-A 5-A 1; 1; DIC	D'aoust M, 2-471503/50. 3 and charact og recombinan
0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	M M M M M M		1 32/c 4D38882 4D38882 3-SEP-2 Ifalfa	xpressi lfalfa; edicagc 0200236 0-MAY-2 1-OCT-2 1-OCT-2 MEDI-)	Vezina L, D'aoust M, WPI; 2002-471503/50. Isolating and character expressing recombinant
2222 2222 2322 2322 2322 2322 2322 232		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3801		XX XX XX V DR W V PT I W

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Matches
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ID AAV
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                                                                                                                                                                                                                                                                                 δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                       expression requiratory sequence for the expression of recombinant polypeptides and/or RNA. The method comprising producing at least one polypeptides and/or RNA. The method comprising producing at least one oligonuclectide primer allows anplification of genomic sequences upstream of the CDNAs. The method is useful for isolating, characterising and identifying a large number of known and unknown promoters that are active under any desired environmental condition to which a cell may be exposed and not just to the exemplified isolation of promoters that are capable of expression in specific conditions. The methods are also useful for cloning genes from any host, or from a specific tissue with such host, from which a cDNA library may be constructed; for the identification and isolation of analogous promoters, signal peptides and structural genes in several species of multicellular and unicellular organisms and as a high throughput identification system of capilate therapeutic targets. The promoter sequence is alfalfalfa plastocyanin gene coding fragment.
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; KARP-1; Ku86 autoantigen related protein; cancer;
immune deficiency disorder; biliary tract cancer; leucine zipper protein;
cytostatic; immunosuppressant; gene therapy; KARP-1 inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids encoding leucine zipper protein, KARP-1 polypeptide, useful for treating cancer and immune deficiency disorder
                                              The invention relates to a method for isolating and characterising an
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                3529 TTACTATAGGCCACGCTGGTCGACGCCCGGGCTGGTATCTAAGTGTGCACC 3477
                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                     DB 24; Length 3548; 0.0029;
                                                                                                                                                                                                                                                                                                                                                   2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACC
                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                            Sequence 3548 BP; 1112 A; 576 C; 727 G; 1133 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                       Score 45;
                     Example 2; Page 68-69; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Column 51-56; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF31861 standard; DNA; 6078 BP.
                                                                                                                                                                                                                                                                                                     4.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYBR-) UNIV BROWN RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0173914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0064557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                             48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-146208/15.
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB66590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hendrickson EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human KARP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6171857-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF31861;
                                                                                                                                                                                                                                                                                                                             Matches
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AAF31861
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KARP-1 nucleic acid and KARP-1 protein are useful for the treatment and/or diagnosis of diseases such as cancer and immune deficiency disorders. They are useful in combination with a KARP-1 inhibitor that inhibits abuble stranded DNA base repair. Inhibitors of KARP-1 are useful in the diagnosis or treatment of conditions characterised by the loss of KARP-1 activity and in the treatment of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an expansin promoter region from Gossypium hirsutum. This has been sequenced and found to be approximately 2200 bp in length, and is immediately 5' to the cotton fibre expansin coding region. The promoter can be used in cotton transformation by linking it to a gene of interest, thus enabling the modification of transgenic cotton fibre cells.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA containing the promoter of the cotton expansin gene - used for tissue-selective expression of genes that alter cotton fibre
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cotton fibre expansin promoter; transformation; transgenic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                          Length 6078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.0%; Score 41; DB 19; Length 2614; Best Local Similarity 100.0%; Pred. No. 0.048; Matches 41; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                  Sequence 6078 BP; 1806 A; 1301 C; 1392 G; 1543 T; 36 other;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2614 BP; 892 A; 436 C; 401 G; 882 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        9 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCTGAA 52
                                                                                                                                                                                                                                                                                                                                                                                                          44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAT 41
                                                                                                                                                                                                                                                                                        Score 42.4; DB 2
Pred. No. 0.028;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cotton promoter region from an expansin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig la-d; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV40621 standard; DNA; 2614
                                                                                                                                                                                                                                                                                        4.1%;
ilarity 97.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0034914.
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                                                                                                                                                                             e.g. biliary tract cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pear JR, Stalker DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-399143/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CALJ ) CALGENE INC
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9830698-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1998
                                                                                                                                                                                                                                                                                                                                                43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV40621;
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                        Local
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RESULT 4

present sequence is given in a specification relating to an isolated Mutoantigen Related Protein (KARP-1) nucleic acid molecule. The

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Rice; promoter; gene therapy; transcription; monocot; anther; chromosome mapping; gene mapping; antisense technology; plant genetic engineering; ss.
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1 Similarity 71.1%;
69; Conservative
                     20-JUN-2001; 2001WO-NZ00115
                                              20-JUN-2000; 2000US-0598401.
28-NOV-2000; 2000US-0724624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                               WPI; 2002-114583/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                        Perera R, Rice S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention.
                                                                                                                                                           P-PSDB; AAU80754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200181606-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-2002
27-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to promoter sequences from eucalyptus and pine. The present sequence is one such promoter. This sequence is useful for modulating the transcription of DNA sequences of interest. The sequences may also be used to tag or identify an organism or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis; temporally regulated promoter; Pinus radiata; Eucalyptus grandis; Ss; PCR primer.
                                                                                                                                                                                                                                                                                                                                                               Novel promoter sequences useful for modulating transcription of plant DNA sequences of interest and production of polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40.6; DB 21; Length 1038;
Pred. No. 0.037;
0; Mismatches 24; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1038 BP; 298 A; 220 C; 233 G; 287 T; 0 other;
                                                                            Senescence-like protein promoter coding sequence #1.
                                                                                                   Promoter; eucalyptus; pine; gene transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ATGCATATACTGCTGAGAGATAACATCACA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 crgrgraarrcargcragrcaccaraacrrrrcrca 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pinus radiata promoter polynucleotide #20.
                                                                                                                                                                                                                                                              (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Pages 57-58; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                     Perera R, Rice SJ, Eagleton CK;
     AAC62796 standard; DNA; 1038 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK17061 standard; cDNA; 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.18;
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                                                                                                                                                                                                    24-FEB-2000; 2000WO-NZ00018
                                                                                                                                                                                                                             99US-0276599
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                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive material.
                                                                                                                                                                                                                                                                                                                             WPI; 2000-647236/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAB28136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200198485-A1
                                                                                                                                                    WO200058474-A1
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                                                                                                                             Pinus radiata.
                                                                                                                                                                                                                          25-MAR-1999;
30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                            05-OCT-2000
                                                     02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK17061;
                             AAC62796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The invention relates to isolated promoter sequences from Pinus radiata and Eucalyptus grandis, comprising a sequence chosen from leaf., root., and Eucalyptus grandis, comprising a sequence chosen from leaf., root., flower., pollen., bud., meristem-specific promoters or temporally computed promoters such as xylogenesis-specific promoters. The promoter computated promoters used for modifying gene expression in a production of genetic constructs, used for modifying gene expression in a target organism, in particular a plant. The method is useful for modifying expression of a polynucleotide that comprises an intron sequence, through removal of the intron sequence. The method is useful computed structured is useful in growth and development of plants, and cellular responses to external stimulus, such as environmental factors and disease pathogens. The sequences are useful in genome and physical mapping, in positional cloning of genes, in various assays to determine biological activity, to craise antibodies, to isolate corresponding interacting proteins and other compounds, and to quantitatively determine levels of interacting proteins corresponding interacting proteins and other compounds. Sequences ABKI7016-ABKI7125 represent Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                           Novel polynucleotide promoter sequences from Pine and Eucalyptus useful for modifying expression of endogenous and/or heterologous polynucleotides in transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40.6; DB 24; Length 1038;
Pred. No. 0.037;
0; Mismatches 24; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1038 BP; 298 A; 220 C; 233 G; 287 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ATGCATATACTGCTGAGAGATAACATCACAATTCACA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
(GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS IND LTD
                                                                                                                                Eagleton C, Lasham A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 73-74; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice anther-specific promoter #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS15016 standard; cDNA; 598
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01-NOV-2001

Perera JR,

Rice

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The invention relates to isolated promoter sequences from Pinus radiata and Bucalyptus grandis, comprising a sequence chosen from leaf-, root-, flower-, pollen-, bud-, meristem-specific promoters or temporally regulated promoters such as xylogenesis-specific promoters. The promoter polypeptides and their related polynucleotides are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide promoter sequences from Pine and Eucalyptus useful for modifying expression of endogenous and/or heterologous polynucleotides in transgenic plants \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promoter; pine; leaf; root, flower; pollen; bud; meristem; xylogenesis; temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
                                                                                                                                                                                                                                                                            and pine. The present sequence is one such promoter. This sequence is useful for modulating the transcription of DNA sequences of interest. sequences may also be used to tag or identify an organism or its
                                                                                                                                               Novel promoter sequences useful for modulating transcription of plant DNA sequences of interest and production of polypeptides \,
                                                                                                                                                                                                                                                          The present invention relates to promoter sequences from eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.9%; Score 40.4; DB 21; Length 2096; Best Local Similarity 97.6%; Pred. No. 0.065; Matches 41; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCTGA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eucalyptus grandis promoter polynucleotide #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lasham A;
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                 Claim 1; Pages 61-62; 93pp; English.
                                           Eagleton CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 78; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK17075 standard; cDNA; 2096 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eagleton C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2001; 2001WO-NZ00115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2000; 2000US-0598401.
28-NOV-2000; 2000US-0724624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                              reproductive material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-114583/15.
P-PSDB; AAU80760.
                                           Perera R, Rice SJ,
                                                                                    WPI; 2000-647236/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perera R, Rice S,
                                                                                                        P-PSDB; AAB28142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200198485-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK17075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to plant polynuclectide sequences from rice which encode promoter components of the cellular activation and transcription apparatus (5' cis regulatory DNA sequences). The sequences may be used in the modification of gene activation and/or expression in eukaryotes, especially rice and other monocots. They have many applications in polymerase chain reaction (PCR) technology, for the study of gene mapping, in polymerase chain reaction (PCR) technology, for the study of gene function and expression in vivo, specific down-regulation of target genes, and in the production of sense and/or antisense nucleic acids. The present sequence represents rice anther-specific promoter #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTGGAT 63
                                                                                                                                                                                                                                                                                                                                                              promoter sequences (I) useful in plant genetic engineering and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24; Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 598 BP; 174 A; 131 C; 113 G; 179 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Promoter; eucalyptus; pine; gene transcription; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%; Score 40.4; DB 24;
75.8%; Pred. No. 0.031;
ive 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O-methyl transferase promoter coding sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC62810 standard; DNA; 2096 BP
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1B; 47pp; English.
                                                                                                    20000S-217891P.
20000S-218366P.
20000S-227231P.
20000S-237736P.
20000S-253925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.8%;
                                         26-APR-2001; 2001WO-US13544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000; 2000WO-NZ00018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0276599
99US-0146591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   molecular biology studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 75.8
nes 50; Conservative
                                                                                                                                                                                                                                      (AKKA-) AKKADIX CORP.
                                                                                                                                                                                                                                                                                                                     WPI; 2002-041419/05.
                                                                                                                                                                                                                                                                               Lu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200058474-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GCATAT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TAATAT 66
                                                                                                 12-JUL-2000;
13-JUL-2000;
23-AUG-2000;
03-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1999;
30-JUL-1999;
                                                                                  26-APR-2000;
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Query Match

Matches

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05-OCT-2000

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Gaps

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                target organism, in particular a plant. The method is useful for modifying expression of a polynucleotide that comprises an intron sequence, through removal of the intron sequence. The method is useful for modifying growth and development of plants, and cellular responses to external stimulus, such as environmental factors and disease pathogens.
                                                                                                                 The sequences are useful in genome and physical mapping, in positional cloning of genes, in various assays to determine biological activity, to raise antibodies, to isolate corresponding interacting proteins and other compounds, and to quantitatively determine levels of interacting proteins or other compounds. Sequences ABK17016-ABK17125 represent Pinus radiata and Eucalyptus grandis polynucleotides and PCR primers used in the method
genetic constructs, used for modifying gene expression in a
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New phospholipid binding proteins and nucleic acids, useful for modulating plant growth homeostasis, controlling cell expansion and cell division, or producing plants where larger fruits and increased biomass are desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana. The coding region of the BONI gene of Arabidopsis thaliana. The coding region of the BONI gene is given in ABA01256. The BONI gene permits wild-type Arabidopsis plants to maintain a relatively constant size over a wide range of temperatures. Thus, bonl null mutants produce miniature fertile plants at 22 degrees C, but a wild-type phenotype at 28 degrees C. BONI has a direct role in regulating cell expansion and cell division at temperatures lower than those at which Arabidopsis is normally grown. The BONI protein (see AAM50644) contains a cat-dependent phospholipid binding domain and is associated with the plasma membrane. BONI belongs to the copine gene family, which is conserved from protozoa to humans. The invention is directed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BONSAII; BONI; phospholipid binding protein; growth; homeostasis; thermotolerance; transgenic plant; plant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis BONSAI1 (BON1) gene, involved in growth homeostasis.
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                      Score 40.4; DB 24; Length 2096;
Pred. No. 0.065;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                Sequence 2096 BP; 537 A; 535 C; 539 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                       TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                        (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 8A; 78pp; English.
                                                                                                                                                                                                                                                                                                                        3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA91255/c
ID ABA91255 standard; DNA; 2611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-2000; 2000US-213863P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-2001; 2001WO-US20172
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.00,
...hos 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-139899/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grisafi P,
                                                                                                                                                                                                                                            of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200200697-A2.
  production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA91255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hua J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel promoter sequences useful for modulating transcription of plant DNA sequences of interest and production of polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is one such promoter. This sequence is
the transcription of DNA sequences of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                       Gaps
         ABA91256-60), which encode proteins (see AAM50644-48) that are necessary for normal growth, controlling cell expansion and cell division, affecting the size and rate at which the plant grows when exposed to lower temperatures. Transgenic plants are provided that are smaller than the wild-type as a result of inhibition of BON1, BON2, BON3, BAP1 and/or BAL, especially angiosperms and gymnosperms, ornamental plants and turfgrass. Transgenic plants are also provided that are larger than the wild-type as a result of enhancement of BON1, BON2, BON3, and both and a specially crop plants and biomass plants. Modulation of these genes provides increased yield, or growth at a higher altitude or lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to promoter sequences from eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used to tag or identify an organism or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                       Score 40.4; DB 24; Length 2611; Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 411;
isolated BON1, BON2, BON3, BAP1 and BAL nucleic acids (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                        Sequence 2611 BP; 809 A; 429 C; 498 G; 866 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ACTATAGGGCACGCGTGGTCGACGCCCGGGCTGGTATGAAGGTG 48
                                                                                                                                                                                                                                                                                                                                     Sequence 411 BP; 112 A; 118 C; 80 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Promoter; eucalyptus; pine; gene transcription; ds.
                                                                                                                                                                                                                                                                                                                      1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40.2; DB 2
Pred. No. 0.029;
0; Mismatches
                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flower specific promoter coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eagleton CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 53; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC62780 standard; DNA; 411 BP
                                                                                                                                                                                                                                                       3.9%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.9%;
93.3%;
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99US-0146591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                         2.9°
Best Local Similarity 97.6°
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences may also be reproductive material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pine. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-647236/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200058474-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-2000.
                                                                                                                                                                                             temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perera R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC62780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAC62780
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Heparanase; hpa; modulator; heparin-binding growth factor;

region of human heparanase cDNA.

(first entry)

09-JUL-1999

AAX35652 standard; cDNA; 594 BP.

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cellular response; cytokine; cell interaction; plasma lipoprotein; cellular susceptibility; infection; disintegration; neurodegenerative plaque; wound healing; angiogenesis; restenosis; athersolerosis; inflammation; neurodegenerative disease; neutralise; plasma heparin; micrometastasis; autoimmune lesion; renal failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
               AAX35652
                                                                                                                              NAMES OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Bucalyptus grandis, comprising a sequence chosen from leaf., root., flower., pollen. bud-, meristem-specific promoters or temporally requiated promoters such as xylogenesis-specific promoters. The promoter polypeptides and their related polypucleotides are useful in the promoter polypeptides and their related polypucleotides are useful in the production of genetic constructs, used for modifying gene expression in a modifying expression of a polynucleotide that comprises an intron sequence, through removal of the intron sequence. The method is useful for modifying growth and development of plants, and cellular responses to external stimulus, such as senvironmental factors and disease pathogens. The sequences are useful in genome and physical mapping, in positional cloning of genes, in various assays to determine biological activity, to raise antibodies, to isolate corresponding interacting proteins and other compounds, and to quantitatively determine levels of interacting proteins or other compounds. Sequences ABKI7016-ABKI7125 represent Pinus radiate and Europhia grandis polynucleotides and PCR primers used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis; temporally regulated promoter; Pinus radiata; Eucalyptus grandis; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 el polynucleotide promoter sequences from Pine and Eucalyptus useful modifying expression of endogenous and/or heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated promoter sequences from Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40.2; DB 24; Length 411;
Pred. No. 0.029;
0; Mismatches 3; Indels 0;
Sequence 411 BP; 112 A; 118 C; 80 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eucalyptus grandis promoter polynucleotide #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perera R, Rice S, Eagleton C, Lasham A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides in transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 68-69; 121pp; English.
                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                             ABK17045 standard; cDNA; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0598401
2000US-0724624
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eucalyptus grandis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200198485-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2000;
28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer.
                                                                                                                                                                                                                                                                                                    ABK17045;
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                                                                                                                                                      RESULT 11
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New human polynucleotide useful for treating angiogenesis,

Example 8; Page 69; 63pp; English.

restenosis, and inflammation

(FRIE/) FRIEDMAN M M. (HADA-) HADASIT MEDICAL RES SERVICES & DEV. (INSI-) INSIGHT STRATEGY & MARKETING LID.

98WO-US17954. 98US-0109386 97US-0922170

31-AUG-1998;

11-MAR-1999

02-SEP-1997;

Homo sapiens. WO9911798-A1 Vlodavsky I;

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Pecker

Feinstein E,

WPI; 1999-302255/25.

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                                                                     growth factors and cytokines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections or disintegration of neurodegenerative plaques. Heparamase may be useful for conditions such as wound healing, angiogenesis, restenosis, inflammation, neurodegenerative diseases, and viral infections. Mammalian heparamase can be used to neutralize plasma heparin, and anti-heparamase antibodies may be applied for immunodetection and diagnosis of micrometastases, autoimmune lesions,
                                                                                                                                                                                                                                                                                       and renal failure in biopsy specimens, plasma samples, and body fluids. The present sequence represents the 5' sequence of human heparanase
                             activity. The recombinant protein is used as a modulator of heparin-binding growth factors, cellular responses to heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
specification describes a polypeptide having heparanase (hpa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 20; Length 594;
Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 594 BP; 133 A; 134 C; 209 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                       3.9%; Score 40; DB
larity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA75054 standard; cDNA; 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA75054;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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AAA75054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Gaps

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48

4 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTG

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Conservative

Local Similarity

42;

Matches

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08-SEP-2000

Pecker I,

NAME OF THE PROOF OF THE PROOF

(FRIE/)

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Seed-preferred promoter; maize; end gene; endosperm; end1; end2; fatty acid; starch profile; carbohydrate profile; amino acid content; agronomic; insect resistance; disease resistance; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the DNA of the invention, and can act as a promoter for the hyaluronate synthase gene. It was isolated from human cDNA sources. The DNA is useful for screening a drug enhancing or inhibiting production of hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a seed-preferred promoter isolated from maize endosperm specific genes, endl or end2. The promoter is capable of
                                                                                                                                                                                                                                                                                                      promoter for hyaluronate synthase gene - used for screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize promoter driving transcription in a seed-preferred stably transforming plant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linnestad C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1680 BP; 452 A; 381 C; 467 G; 380 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.9%; Score 40; DB 20; L 100.0%; Pred. No. 0.077; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CITACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seed-preferred promoter-2 from maize end gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                                                                                              (ADSK-) ADVANCED SKIN RES KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Pages 35-36; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 5-6; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martino-Catt SJ, Lappegard KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ51547 standard; DNA; 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0098230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US19604
                                                                                                                            97JP-0107624
                                                                                                                                                                       97JP-0107624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.9
Best Local Similarity 100.
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   grain characteristic; ds
                                                                                                                                                                                                                                                                                                                             modulators of the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-256648/22.
                                                                                                                                                                                                                                                            WPI; 1999-038280/04.
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Homo sapiens.
                                                                                                                                                                       24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1998;
                                         JP10295383-A
                                                                                                                              24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2000.
                                                                                  10-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ51547;
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ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is an upstream sequence of CDNA encoding encodes a human protein with heparanase catalytic activity. The heparanase (hpa) polynucleotide is useful in gene therapy, particularly in treating tumour, inflammation or autoimmunity. Particularly, the polynucleotide is useful in modulating the bioavailability of heparin-binding growth factors, cellular responses to heparin-binding growth factors (e.g. interleukin (Il)-8), cell interaction with plasma and cytokines (e.g. interleukin (Il)-8), cell interaction with plasma inpoproteins, cellular susceptibility to certain viral and some bacterial and protozoa infections, or disintegration of neurodegenerative plaques. The polynucleotide is also useful in wound healing (e.g. thermal, chemical or radiation burns), and in the treatment of angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-Straussler Syndrome or Creutzfeldt-Jakob disease), and some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding a polypeptide having heparanase activity, useful in wound healing and in gene therapy, particularly in treating tumour, inflammation, autoimmunity, neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                     autoimmunity;
                                                                                  Human; heparanase; gene therapy; tumour; inflammation; autoimmunit; heparin-binding growth factor; cytokine; neurodegenerative plaque; wound healing; infection; burn; amplogenesis; restenosis; atherosclerosis; inflammation; neurodegenerative disease; Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.9%; Score 40; DB 21; Length 594;
100.0%; Pred. No. 0.041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 594 BP; 133 A; 134 C; 209 G; 118 T; 0 other;
                                           Upstream sequence of human cDNA encoding heparanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGTAT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           (INSI-) INSIGHT STRATEGY & MARKETING LTD. (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyaluronate synthase; promoter; human;
hyaluronic acid production inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral, bacterial or protozoa infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 127; 152pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feinstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV08328 standard; cDNA; 1680 BP
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                                                                                                                                                                                                                                                                                                                                                        14-FEB-2000; 2000WO-US03542.
                                                                                                                                                                                                                                                                                                                                                                                                  99US-0258892
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  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vlodavsky I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRIEDMAN M M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-579289/54.
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nes 40; Conserv
                                                                                                                                                                                                                                                                 WO200052178-A1
                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1999;
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15-JAN-2001
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Gaps

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Indels

Length 1680;

manner, for

AAV08328

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RESULT 14

Query Match

Best Loc Matches

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driving transcription in a seed-preferred manner and can be used in an expression cassette, to stably transform plant cells. The expression cassette can be used to modify the fatty acid content of seeds, alter the starch or carbohydrate profile, and/or alter the amino acid content of the seed. It can also be used to deliver genes encoding important traits for agronomics, including insect resistance, disease resistance, herbicide resistance, and grain characteristics.
      888888888
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Sequence 1224 BP; 378 A; 239 C; 182 G; 425 T; 0 other;

0; Gaps ; 0 Score 39.8; DB 21; Length 1224; Pred. No. 0.074; 0; Mismatches 2; Indels 0; Query Match 3.9%; Best Local Similarity 95.3%; Matches 41; Conservative

45 3 TACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAG

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Search completed: December 28, 2002, 00:07:43 Job time: 254 secs

Database

Searched:

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Pred. No. is the number of results predicted by chance to have a

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em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	F429315 Homo si F429315 Homo si L773534 Mus mus F457660 Castan F039526 Homo si R124194 Sequent	AALA119 Judence Continuation (4 of Continuation (3 of AY124482 Danio rer AF051769 Home sapi AF075270 Hordeum v AL133378 Human DNA AL031655 Human DNA AX320057 Sequence AY153014 Trichomon	AR021922 Homo sapi AC025822 Homo sapi US3907 Rattus norv . AF233737 Agrotis i AX253428 Sequence AX1514032 Wus muscu AX041981 Sequence	uenc s mu omo omo eque el p hrli hrli eque eque eque	9 Homo 1 Rattu 6 Sinox 7 Sinox 11 Casta 2 Seque 9 Seque 6 Mus n
SUMMARIES	AF42931 AF42931 AL77353 AF45766 AF03952	ARIZ4194  ARIZ4191-3  PFMAL4P1-3  PFMAL4P1-3  ARIZ4482  ARIZ4769  ARO5270  ARI39378  HSI34N8  AX320057	AX38000 AC025822 AC025822 AF03337 AX23337 AX253428 AX253428 AX053428 AX041981	AX34456 166494 MMUG38 AX09843 AX09843 AX2005 AF23741 AX32005 AX32005 AX1628 AC08788	ACO2 AC10 SME5 SME5 AX68 AX08 AX08 ACO7
DB				6 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
Le	12502 12502 12502 21687 681 142	92633 110000 4260 11957 11657 16603 156325 156325	220031 220031 498 951 985 1499 1958 682 2385	349980 7218 640 1640 2493 2867 2867 4185 516 615 2785 104526	149440 196049 299350 329100 1157 5031 5031 180968
% Query Match	. B E E C I I -			$\begin{matrix} \omega_1 & \omega_2 & \omega_3 & \omega_4 & \omega_5 & \omega_$	
ore	4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		4 4 4 4 4		8 8 8 8 8 9 9 9 9 8 8 8 8 8 8 8 8 8 8 8 8
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c aF429315 125020 bb DNA linear PRI 18-JAN-2002	Homo sapiens junctophilin 3 (JPH3)		Homo sapiens.			
RESULT 1 AF429315/C	DEFINITION	VERSION	SOURCE	ONGRINTON	REFERENCE AUTHORS	

944 CGCCATCAGTAGCACCGGCA 963

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HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWYKGEWTHGFRGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="component of the junctional complex between plasma membrane and endoplasmic reticulum"
                                                                                                                          2 (bases 1 to 125020)
Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
Submitsed (05-0CT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17666 WSSYSTSMGYYSSTSCKYYKCSWSSMYKCKTSKSYRRKRSYYYWGGGKRAKKKYYCAGRR 17607
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A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                             /map="16924.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
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complement(<36507. .>36887)
/gene="JPH3"
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complement(<36507. .36887)
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/protein_id="AAL40941.1"
/db_xref="G1:17646245"
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/rpt_type=tandem
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                              /chromosome="16"
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/product=iunctophilin 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 125020)
Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 (4), 377-378 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      # Clades S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission

Submitted (05-007-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA Location/Qualifiers

1. 125020

/ Organism="Homo sapiens"
/ /db_xref="taxon:9606"
/ /chromosome="16"
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/note="1solated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
/rpt_type=tandem
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HOMO sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
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complement(<36507, .36887)
/gene="JPH3"
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/gene="JPH3"
17246 NRRNNRMGKTGCNYMYRRSR 17227
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Best Local Similarity
Matches 53; Conserv
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AF457660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL773534 216878 bp DNA linear HTG 17-AUG-2002 Mus musculus chromosome 2 clone RP23-183012, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 216878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk on Aug 21, 2002 this sequence version replaced gi:220027033.
                          50699 GVHTGVMRWVGYGBCDTHVTYDGGHHGSWGMMKSCGYSDBGKCAKBGSKMCTGSMTKYTC 50758
                                                                                                                     50819 YVKYBSMSVSARKSKGHKVYBSSMKCSRRKDMSTSSMWRSMKDRKCSRCSHSHYSKSMGK 50878
                                                                                                                                                                                                                                                                                                          50939 MVDKSRRRMKGSAMRGMKCYCYTSSMRSTKSRSMKSSWRWGSKCYYCYGYWSCTKWRSMG 50998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 706 TGCCAACCAGACCTGGCATGGCCTGGTGGCGTCATCTAATTTCTCCTATCAAAGAATCAC 765
                                                                                                                                                                                                                                                                                                                                                                            826 CAGGCACCACCGCCATCAAATACGGCCTCTTTGCGGCACGGATCTGCACCGACGGGC 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator: 100% of reads
Consensus quality: 216591 bases at least 040
Consensus quality: 216754 bases at least 030
Consensus quality: 216766 bases at least 030
Insert size: 216778; sum-of-contigs
Insert size: 216778; serior: agarose-fp
Ouality coverage: 7.01x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886 GCAATTGAATTCGAGCCTGATCGAGGTGGTTGGATCGCGCAGGGAAACCTTGAATGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
  590 TGTCTCCAACTCTGCATTTTCGGTTCAGAGCAG----TACTGCATTTTGCCATTGTCGCC
                                                                                          766 CTCCCATTACTCCGCCCTGTGCGGCGACCTCGTGCCCTCGAATTCCACGGGCACACGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51059 RSGRMSAYCSCRKCKSKRCSGCMRCSWYCWYKCMRYGSWRMYKC 51102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATCAGTAGCACCGCCACGTCACCTCTGAAGAAGAGCTGTCGC 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coverage: 7.25x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .... Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: bM183012
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VERSION
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AL773534
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Castanea dentata clone ACS2 vascular protein gene, promoter region. AF457660
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I (bases I to 685)

Connors, B.J., Maynard, C.A. and Powell, W.A.
Cloning and characterization of promoters from American chestnut capable of directing reporter gene expression in transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUNY-ESF, 1 Forestry Drive, Syracuse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 137585 ATTTGCATTTGATGAACTGTCTTTATTTTTAAATGATTAGAAATAGTACATTTAAAAGGA 137644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 137525 AATTGTCTAAAATAAGCAAAATTACAAGATTGACTATATACTTCCCTCTGTATTAGTT 137584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 ATTITIATCICCCCAACCGCCATIAGIAAGCAGGCCCCCCAACGCATTCAAATICGATGIA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 ATTGTCTACTTCATTTTGGTTCAGATTTGAACGATGTCAGTTTCAATCCACATGCAACAG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AAGAATGTGGATTACAACAGTTCTATCTGAGCGACAGTCTAAACGCAGCTTTGTATAGTC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 AATCCGCAGAAGAATTCATCCAATTCACATAAAGCAGCAACAGAAGTTAAACCATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 216878;
                    15292 15391: gap of _ 100 bp
15392 216878: contig of 201487 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                              100 others
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15291: contig of 15291 bp in length
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Connors,B.J., Maynard,C.A. and Powell,W.A.
Direct Submission
Submitted (12-DEC-2001) EFB, SUNY-ESF, 1 F
NY 13210-2788, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44.4; DB 2;
Pred. No. 0.31;
0; Mismatches 146;
                                                                                                                                                                                       /clone="RP23-183012"
/clone_lib="RPCI-23"
| . 15591
| /note="assembly_fragment:02090
fragment_chain:1"
15392 . 216878
framment chain:1"
framment chain:1"
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/db_xref="taxon:134033"
/clone="ACS2"
                                                                                                                                                                                                                                                                                                                                                                                              41503 g 63544 t
                                                                                               1. .216878
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            |ragment_chain:|
| 41471 c | 41503
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Castanea dentata
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PAT 16-MAY-2001

linear

36 others

1543 t

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1 (bases 1 to 6078)
Hendrickson, E.A.
Leucine zipper protein, KARP-1 and methods of regulating DNA dependent protein kinase activity
Patent: US 6171857-A 1 09-JAN-2001;
Location/Qualifiers
             CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCTGAA
                                                                                6078 bp
Sequence 1 from patent US 6171857.
AR124194.1 GI:14109555
                                                                                                                                                                                                                                                                                              /organism="unknown"
1301 c 1392 g
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200001
300001
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Best Local Similarity
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Best Local Similarity
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PFMAL4P1_2
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PFMAL4P1_3/c
WPCOMMENT
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PFMAL4P1_2/c
WPCOMMENT
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ORIGIN
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                                                                                                            ACCESSION
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TITLE
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                                                     RESULT 6
AR124194
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Homo sapiens MHC class I related protein 1 (MR1) gene, partial cds.
AF039526
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1 (bases 1 to 1423)
Riegert, P., Wanner, V. and Bahram, S. Genomics, isoforms, expression, and phylogeny of the MHC class I-related MRI gene
J. Immunol. 161 (8), 4066-4077 (1998)
98451457
                                                                                                            Gaps
                                                                                                                                  1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTG 60
                                                                                                                                                  Gaps
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Riegert, P., Wanner, V., Hauptmann, G. and Bahram, S.
Direct Submission
Submitted (22-28C-1997) EG, Basel Institute for Immunology,
Grenzacherstrasse 487, Basel 4005, Switzerland
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                                                                             Score 42.8; DB 8; Length 685;
Pred. No. 0.31;
0; Mismatches 37; Indels
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                                                                                                       37; Indels
                      protein promoter region"
7 q 189 t
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/evidence=not_experimental
1390. .>1423
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                                                                                                                                                                                          61 GATGCATATACTGCTGAGAGATAACATCACAATTCACAAGCT 102
                                                                                                                                                                                                            .,
6
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/product="Mtc class I related
/protein_id="AAAD02172.1"
/db_xref="GI:4104808"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.1%; Score 42.4; DB ilarity 97.7%; Pred. No. 0.47; Conservative 0; Mismatches
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334 c 310 q 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q25"
1. >1423
1. .685
/note="vascular pro
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/codon_start=1
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                                                                           ch 4.2%;
1 Similarity 63.7%;
65; Conservative
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Best Local Similarity
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Matches 65; Conserv
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AUTHORS
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AF039526
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PFMAL4P1_3 300001 392633
Continuation (4 of 4) of PFMAL4P1 from base 300001 (AL034557 Plasmodium falciparum 3D
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                                                                                                                                                                                                 LOCUS PFMAL4P1 Accession AL034557
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Pred. No. 1.6;
0; Mismatches 32; Indels 0;
                                  ó;
                                                                                                                                                                                                                                                                                                                                   Length 92633;
 Length 6078;
                                Indels
                                                                                                                                                                                                                                                                                                                                                               32; Indels
                                                                                               52
                                                                 44
                                                                                 9 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCGAA
                                                                1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAA
                                1;
                                                                                                                                                                                                                                                                                                                                 DB 2;
   9
Score 42.4; DB
Pred. No. 0.62;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                Score 41.8; DI
Pred. No. 1.6;
0; Mismatches
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310000
392633
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210000
310000
392633
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                                                                                                                                                                                                Sequence split into 4 fragments
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PFMAL4Pl_2 200001

PFMAL4Pl_3 300001

Continuation (3 of 4) of PFMAL4Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence split into 4 fragments
ch 4.1%;
1 Similarity 97.7%;
43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%;
                                                                                                                                                                                                                                                                                                                              ch 4.1%;
1 Similarity 65.6%;
61; Conservative
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...v.zevv
Hordeum vulgare high affinity sulfate transporter (HVST1) gene,
promoter region, 5'UTR, and partial cds.
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.

( pases I to 1094)
Vidmar,J.J., Schjoerring,J.K., Touraine,B. and Glass,A.M.D.
Regulation of the HySTI gene encoding a high affinity sulfate transporter from Hordeum vulgare
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 11957)

Csoka, A.B., Scherer, S.W. and Stern, R.

Expression analysis of six paralogous human hyaluronidase genes clustered on chromosomes 3p21 and 7q31

Genomics 60 (3), 356-361 (1999)
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Vidmar,J.J., Schjoerring,J.K. and Glass,A.M.D.
Direct Submission
Submitted (30-JUN-1998) Botany, University of British Columbia, 6270 University Blvd., Vancouver, B.C. V6T1Z4, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hyaluronidase-like pseudogene 1; exon/intron structure not yet determined"
                                                                                                                                                                                                                                                                    Submitted (28-FEB-1998) Pathology, University of California, Parnassus St. at 3rd Ave, San Francisco, CA 94143, USA
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/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Klondike"
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illarity 100.0%; Pred. No. 1.8;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. 11957
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7931.3"
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2244 c 2085 g
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/gene="HYALP1"
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1025. .>1094
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Direct Submission
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                    Homo sapiens.
                                        Homo sapiens
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Matches 41; Conserv
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PUBMED
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AF075270
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KEYWORDS
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                                                                                                                                                                            A1124462 4260 bp DNA linear VRT 31-JUL-2002 bando rerio myogenin gene, exons 1, 2 and 3 and complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF051769 11957 bp DNA linear PRI 31-OCT-1999
Homo sapiens hyaluronidase-like pseudogene l (HYALPI), partial
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                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Oyprinidae; Danio.

1 (bases 1 to 4260)

Du, S., Gao, J. and Anyangwe, V.

Muscle-specific expression of myogenin in zebrafish embryos is
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Muscle-specific expression of myogenin in zebrafish embryos controlled by multiple regulatory elements in the promoter
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                                                                        4.0%; Score 41; DB 5
89.8%; Pred. No. 1.5;
tive 0; Mismatches
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                                                    61 GATGCATATACTGCTGAGAGATAACATCACAAT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="myogenin"
/protein_id="AAM82616.1"
/db_xref="GI:22035405"
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/organism="Danio rerio"
/db_xref="taxon:7955"
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Du,S., Gao,J. and Anyangwe,V.
Direct Submission
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AY124482.1 GI:22035404
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AF051769
AF051769.1 GI:6164589
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3002. 3599
/number=3
a 797 c
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Best Local Similarity 89.89
Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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AF051769/c
LOCUS
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AY124482/c
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.466 of consensus"

.138 of consensus"

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5'UTR

CDS

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/translation="MESSAKIVKPNDEKPDEFESGISQALLELEMNSDLKAQLRELN
ITAAKEIELGGGRKAIIIFYPIPQLKSFOKIQVRLYRELEKKFSGKHVVFIVORRILP
KPTRKSRTKNGKRRPRSHTLTAVHDAILEDLVFPSEIVGKRIRVKLDGSRLIKVHLDK
AQQNNVEHKVETFSOYYKKLIGKDVRFEFPEFQLQTKWHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       match: ESTS: Em:AA105661 Em:A1462024
match: proteins: Tr:092NS1 Sw:Q10101 Sw:O43105 Tr:Q9VA91
Tr:Q23312 Sw:P003562 Sw:P23821 Sw:P48155 Sw:P33514
Tr:Q29190 Tr:013167 Sw:P50894"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2933. .3198
/note="LlPA16 repeat: matches 5853. .6157 of consensus"
3250. .3410
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/product="bA271B5.1 (similar to ribosomal protein S7)"
/protein_id="CAC17691.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7766. .7889
/note="FLAM_C repeat: matches 11. .132 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2748 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 1807. .2082 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5493. .5804

Anote-"Aluy repeat: matches 1. .311 of consensus"

6576. .6869

Anote-"Alusc repeat: matches 1. .289 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5016. .5305 /
/note="AluSx repeat: matches 1. .288 of consensus"
                                                                                                                                                                                                                                                                                                         1669. .1922
/note="AluJb repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                      7324. .7630
/note="AluY repeat: matches 1. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                      2320. .2372
/note="L2 repeat: matches 2700. .2750 of
                                                                                                                                                                                                                                                                                                                                                                                                           2621. .2932 /
/note="MLTIC repeat: matches 147.
                                                                                                                                                                                            463. 580
/note="MER5A repeat: matches 17.
1191. 1400
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/note="MSTC repeat: matches 291.
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                                                                                                                                                       27. .485
/note="match: GSS: Em:B83261"
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/gene="bA271B5.1"
                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                          /clone_lib="RPCI-11.1"
                                                                                                    /clone="RP11-271B5"
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10995. .11131
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10997. .11430
/note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lucial Submitted (18-Jul. 2000) Sanger Centre, Hinxton, Cambridgeshire, Cauminited (18-Jul. 2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquestessanger.ac.uk
on Jun 4, 2000 this sequence version replaced gi:8246895.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve alls sequencing problems, such as compressions and repeats, but not necessarily within known annotated human, repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Emr., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORNPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping Group. Further information can be found at http://www.xanger.ac.uk/HGPP/Chr13. RPI1-271B5 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA sequence from clone RP11-271B5 on chromosome 13 Contains a gene for a protein similar to ribosomal protein S7, the FGF9 (fibroblast growth factor 9 (glia-activating factor)) gene, ESTS, STSS, GSSs and CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                      4.0%; Score 40.8; DB 8; Length 1094; llarity 95.5%; Pred. No. 1.3; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                         /product-"high affinity sulfate transporter"
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/db xref="G1:3643824"
/translation="MP"
  product="high affinity sulfate transporter"
1025. .1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCTGCA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
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                                                                                                                                                                                                                                                                                    243 g
                                             1025. .1089
/gene="HVST1"
1090. .>1094
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/codon_start=1
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'gene="HVST1"
                                                                                                                                                                                                                                                                                 261 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blakey,S.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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ORGANISM

SOURCE

ACCESSION VERSION KEYWORDS AUTHORS TITLE JOURNAL

COMMENT

FEATURES

REFERENCE

Query Match

Best Loca Matches

AL139378/c DEFINITION

RESULT 12

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BASE COUNT ORIGIN

consensus

.359 of

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complement_states 2397. .2697 of consensus"
//note="match: GSS: Em:AZ023172"
28519. .28686
//note="match: GSS: Em:AQ559377"
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29406. .29491
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//note="LIPA5 repeat: matches 5740. .6145 of consensus"
//note="LIPA5 repeat: matches 5740. .6145 of consensus"
//note="LIPA5 repeat: matches 5740. .6145 of consensus"
//note="matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19742. 19834

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19863. 20033

100025. 20038 repeat: matches 1. .138 of consensus"
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/note="MER2 repeat: matches 1. .345 of consensus"
13779. 13979. 13979. 13979. 13970. 13970. 13970. 13970. 13970. 13970. 10040. 14294
/note="LiM4c repeat: matches 1260. 1464 of consensus"
15515. 15827
                                                                                                                                                                                    /// Anotes | MITZFA repeat: matches 96. .128 of consensus | 32843. .33060 | Anotes | MITZFA repeat: matches 121. .349 of consensus | 33068. .33143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ377301"
31396. 31605
/note="MLTSC repeat: matches 228. 386 of consensus"
31899. 32195
/note="Alux_repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluSx repeat: matches 6. .269 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .303 of consensus"
                                                                                                                                                               .188 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluY repeat: matches 1. .303 of consensus"
16476. .16517
/note="14 copies 3 mer tta 78% conserved"
16651. .16946
/note="AluSq repeat: matches 1. .296 of consensus"
17442. .17709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18944. 19037
//note="WR repeat: matches 49. .143 of consensus"
19023. 19447
/note="match: GSS: Em:AQ630744"
                                                                                                                                   /note="MER5A repeat: matches 3.
11884, .12154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19036. .19496
/note="match: GSS: Em:AQ630723"
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/note="Alux repeat: matches 1.
12786. .32818
                            Em: AQ264373"
                                                                                            /note="match: GSS: Em:AQ554409"
11672. .11854
                            /note="match: GSS:
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Assuming the Worker Submission

Loud (16-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 185A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequesr@sanger.ac.uk compared gis5860979.

On Jan 26, 2001 this sequence version replaced gi:5360979.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases:

Em.; EMBL; Sw.; SWISSROT; Tr.; TREMBL; Wp.; WORWFEP; Information on the WORMFEP database can be found at the WORMFEP database can be found at the WORMFEP database can be found at conting of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at the Library RFQ-134NB is from the library RFQ-1 constructed by the group of Pieter de Jong. For further details see human warmen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the entire insert of clone RP1-134NB The true left and of clone RP5-1007PB is at 84660 in this sequence. The true right end of clone RP5-91364 is at 91640 in this sequence. This sequence was finished as follows unless otherwise noted: all sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HS134N8 110-MAR-2001 Human DNA sequence from clone RP1-134N8 on chromosome 20pl2. Contains STSs, GSSs and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156325)
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                                                                                                                                                                                                                                                                                                                                                                                303 TACTICALITIGGILCAGAITIGAACGAIGICAGITICAATCCACATGCAACAGAAICCG 362
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                       Length 166703;
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0
/note="19 copies 4 mer ctct 65% conserved"
33069. .33140
/note="36 copies 2 mer tc 65% conserved"
33401. .33472
/note="18 copies 4 mer atat 81% conserved"
33402. .33473
                                                                                                                                                                                                                                                                                                                67; Indels
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4.0%; Score 40.8; D.
Best Local Similarity 54.7%; Pred. No. 3.5;
Matches 81; Conservative 0; Mismatches
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AL031655.8 GI:12545137
HTG; CpG island.
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[Anotes"LIMB8 repeat: matches 5379. .6171 of consensus" [10898. .11043]
[Anotes"AluJb repeat: matches 159. .305 of consensus" [11097. .11191]
[Anotes"LIMB8 repeat: matches 5276. .5374 of consensus" [1097. .11191]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0040. .6834 '
note="LIPA3 repeat: matches 5351. .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                              1847. .4897
/note="LIMEc repeat: matches 1318. .1368 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6155 of consensus"
                                                                                                                                                                                                                                                                                                                    /note="3 copies 20 mer 90% conserved"
4422. .4603
/note="HAL1 repeat: matches 579. .771 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12638. .12711
/note="37 copies 2 mer tt 67% conserved"
12921. .13046
/note="FLAM_A repeat: matches 1. .127 of consensus"
14487. .14958
/note="12 repeat: matches 2225. .2749 of consensus"
15346. .15405
                                                                                                                                                                                                                                                                                                                                                                                                                  1904. .5263
'note="LTR18A repeat: matches 1. .603 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MERSA repeat: matches 17. .100 of consensus" 17529. .17978 //note="match: GSS: Em:AQ231626" //note="match: 17852. .18269 //note="MSTB repeat: matches 2. .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8809. .8924
/note="MIR repeat: matches 119. .230 of consensus" 9121. .9280
/note="MIR repeat: matches 45. .206 of consensus"
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note="Alusx repeat: matches 1. 312 of consensus"
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note="MERSB repeat: matches 2. .133 of consensus"
[7481, .17553
                                                                                                                                                         1278. 1446
//note="MRR3 repeat: matches 1. .171 of consensus" 1686. 1846
//note="MIR repeat: matches 29. .179 of consensus" 2396. .2495
//note="5 copies 20 mer 75% conserved" 2400. .2485
//note="43 copies 2 mer 47% conserved"
                                                                                                                                              .136 of consensus'
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/note="123 copies 2 mer tt 54% conserved"
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5357. .15404
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/note="LIME3 repeat: matches 5802.
8809, .8924
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fnote="match: GSS: Em:AQ228387"
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'note="match: GSS: Em:B66714"
                                                                     /map="pl2"
/clone="RP1-134N8"
/clone_lib="RPCI-1"
/lu5. .1261
/note="MER5A repeat: matches
1. .156325
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                    /chromosome="20"
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/note="3 cop
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Search completed: December 27, 2002, 23:39:23 Job time : 3391 secs
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                         Db 151285 AGTTTTATTTTAAATAAACATATTTTAATGTATGAAATTTGCTAATTTAAAGAAAAATCT 151344
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                                                                                                                                                                                    0; Gaps
                                     .541 of consensus"
/note="L2 repeat: matches 2577. .2710 of consensus" 39012. .39140
/note="MLT1H repeat: matches 339. .541 of consensus'complement(40115. .40665)
/note="match: GSS: Em:AQ424883"
40161. .40298
/note="L2 repeat: matches 2605. .2750 of consensus"
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Trichomonas vaginalis
Eukaryota, Parabasalidea; Trichomonadida; Trichomonadidae;
Trichomonadinae; Trichomonas.
                                                                                                                                            Query Match 3.9%; Score 40.6; DB 9; Length 156325; Best Local Similarity 55.2%; Pred. No. 4; Matches 79; Conservative 0; Mismatches 64; Indels 0;
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Trichomonas vaginalis Tvp14 (tvp14) gene, complete cds.
AF153014
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Polynuclectide sequences from rice
Patent: Wo 0181606-A 14 01-NOV-2001;
Akkadix Corporation (US)
Location/Qualifiers
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Sequence 14 from Patent WO0181606.
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/db_xref="taxon:4530"
131 c 113 g 179
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1 (bases 1 to 1463)
Crouch,M.V. and Alderete,J.F.
Trichomonas vaginalis has two fibronectin-like iron-regulated genes
Arch. Med. Res. 32 (2), 102-107 (2001)
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/protein_id="AAF73223.1"
/d_xxef="f=g1:8132115"
/translation="WATEEFTYDLLSRHEVIAEFQGLQHIPCRFWTSLCPDRCDHATD
VALFKVLEYTKYEKPGEFGDPKHETIYVDVKKKVFNQDPKIQEYCKTLEVGKKYRVCY
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                                                                                                                          2 (bases 1 to 1463)
Crouch,M.-L. and Alderete,J.F.
Direct Submission
Submitted (19-MAY-1999) Microbiology, UTHSCSA, 7703 Floyd Curl Dr,
San Antonio, TX 78284-7758, USA
Location/Qualifiers
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    1463
    /organism="Trichomonas vaginalis"

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242 c 233 g 46
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796. .1173
/gene="tvp14"
796. .1173
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Matches 41; Conserv
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SALK\_0469 SALK\_0180 SALK\_0103

Drosophil SALK\_0002 SALK\_0118 SALK\_0080 SALK\_0473 SALK\_0473

BH610787 BH214178 ALO68402 BH168812 BH251572 BH212774 BH749138

BH748887 BH610787 BH214178 CNS00LGU

SALK\_0109 SALK\_0146 SALK\_0408 SALK\_0328 SALK\_0328 SALK\_0328

BH172739 SBH251074 BH253202 S

BH172739 BH251074 BH253202 BH750440

BH750440

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Sosidae; eurosidas II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 380)

2 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Gaske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Nabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute Genomic Analysis Laboratory (SIGNAL)

This single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                 BH747511 388 bp DNA linear GSS 27-FEB-2002 SALK_018023.45.85.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_018023.45.85.x, DNA
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BH747511.1 GI:18960626
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Arabidopsis thaliana
VERSION
KEYWORDS
SOURCE
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December 27, 2002, 19:37:43 ; Search time 1965 Seconds (without alignments) 8489.237 Million cell updates/sec
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                                                                                                                1 cttactatagggcacgcgtg......tgtatatacaaggtctgg 1030
                                                                                                                                                                               32308132
       GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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SALK\_0026 SALK\_0140 SALK\_0358

BH616998 BH752369 BH170998 BH611050 BH611042

BH752369 BH170998 BH611050

вн616998

SALK\_0165

SALK\_0315 SALK\_0123 036\_P\_10-T3 end of SALK\_0059

BH252514 BH611714 BH251902 BH188842 AL625781 BH172612 BH250920 BH251621

CNS07SRN BH172612 BH250920

BH251621

BH251902

SALK\_0297 SALK\_0297

SALK\_0135

SALK\_0107 SALK\_0118

ALIGNMENTS

JOURNAL COMMENT

Description

BH747511 SALK\_0180 BH251364 SALK\_0114 BH617520 SALK\_0372 BH613783 SALK\_0349 BH250931 SALK\_0107 BH634101 SALK\_0447

BH251364 BH617520 BH613783 BH250931 BH634101

388 469 111 124 384 445

43.6 43.4 42.8 42.8

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BH747511

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DB

Query Match Length

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SALK\_0362 SALK\_0031 SALK\_0473 SALK\_0109 SALK\_0162 SALK\_0045 SALK\_0180

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BH617520/c
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A Simmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Unpublished (2001)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Email: ecker@salk.edu
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                                                                                                                                                                                                                                         each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html* 95 c 82 g 110 t 3 others
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
                                                                                                                                                                       /clone="SALK_018023.45.85.x"
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/note="PCR was performed on Arabidopsis thaliana lines
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Pred. No. 0.0094;
0; Mismatches 15; Indels
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/organism="Arabidopsis thaliana"
                                                                                                            /organism="Arabidopsis thaliana"
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TDNA. This sequence
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Posidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 111)

2 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 120 c 81 g 135 t 40 others
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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/clone_PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html*
21 c 31 g 28 t
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4.4%; Pred. No. 0.018;
ve 0; Mismatches 36;
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Pred. No. 0.028;
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Best Local Similarity 84.5%;
Matches 49; Conservative
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BH634101 445 bp DNA linear GSS 01-FEB-2002 SALK_044702 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_044702, DNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicacea; Arabidopsis.

1 (bases 1 to 445)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_010743"
/clone=lib="Azhabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which conteains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torray Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                             Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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/organism="Arabidopsis thaliana"
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4.2%; Score 42.8; Di
Best Local Similarity 75.7%; Pred. No. 0.04
Matches 53; Conservative 0; Mismatches
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Fax: 858 558 6379
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                                                                                                                                                                                                                                                                                        ecker@salk.edu
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                   SALK_034950 Arabidopsis thaliana TDNA linear GSS 04-JAN-2002 thaliana genomic clone SALK_034950, DNA sequence.
BH613783
BH613783.1 GI:18063245
GSS.
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Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 384)
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A Sequence-Indexed Library of Insertion Mutations in the
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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ilarity 63.7%; Pred. No. 0.029;
Conservative 0; Mismatches 37;
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/db_xref="taxon:3702"
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Arabidopsis thaliana
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 440)
Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C.J. Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
                                                                                                                                                                                                                                     directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 129 c 86 g 115 t 1 others
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/clone="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
                                                                                                                                                      /clone_lib-"Arabidopsis thaliana TDNA insertion lines /note-"PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was
This sequence lies within an annotated exon of At1g16780
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological Studies
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/db_xref="taxon:3702"
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                                     Location/Qualifiers
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1 Similarity 75.7%;
53; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ecker@salk.edu
                      tagged
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Tobases 1 to 432)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R., Farnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
This is single pass sequence recovered from the left border of TDNA, This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALK 018043 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_018043, DNA sequence.
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insertion. Details of the protocols used can http://signal.salk.edu/tdna_protocols.html" 111 g 104 t
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/clone="SALK_O18043"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/note="Perk was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
elements. The resultant fragment for each line was
firectly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Similarity 74.6%; Pred. No. 0.075;
33; Conservative 0; Mismatches 18;
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Pred. No. 0.
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Best Local Similarity 67.4%;
Matches 60; Conservative
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208 g
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A Sequence Indexed Library of Insertion Mutations in the
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//clone="SALK_010362"
//clone="SALK_010362"
//clone_lib="Arabidopsis thaliana TDNA insertion lines"
//note="PCR was performed on Arabidopsis thaliana lines
ach of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                             500 bp DNA linear GSS 24-OCT-200 SALK_010362 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_010362, DNA sequence.
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
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AL068402
AL068402.1 GI:4958457
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                                                                                                                                                                                                                                               thale cress.
Arabidopsis thaliana
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Matches 50; Conserv
 64 GCATATACTGC
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

By 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkely Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw 9p, the same strain used for the BDGP's and how to order individual BAC Clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Klm,C.J., Parker,H., Prednis,L., Shinn,P.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neptera; Endoptera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="RPCI-98"
/note="end : T7"
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source

FEATURES

BASE COUNT ORIGIN

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ACCESSION

KEYWORDS

SOURCE

VERSION

RESULT 12

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

JOURNAL

COMMENT

TITLE

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BHZ12774 452 bp DNA linear GSS 24-OCT-2001 SALK_008030 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_008030, DNA sequence.
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/clone="SALK_008030"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
a 113 c 111 g 93 t 21 others
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Albaso, W., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, W., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J. R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                  4.1%; Score 42; DB 17; Length 220; llarity 73.0%; Pred. No. 0.067; Conservative 0; Mismatches 20; Indels
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                     /organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
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     Location/Qualifiers
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Class: TDNA tagged
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Best Local
                                  source
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BH212774/C
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Matches
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     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                     /crganism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="Laxon:3702"
/clone="SALK_000215"
/clone="SALK_000215"
/clone="SALK_000215"
/clone="SALK_000215"
/clone="In a performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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SALK_011803 Arabidopsis thallana TDNA insertion lines Arabidopsis
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
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S Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrin, C.J., Gake,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shin, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 17; Length 129;
Pred. No. 0.054;
0; Mismatches 35; Indels
                                                                                                                      Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 888 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana genomic clone SALK_011803, DNA sequence.
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1. .129
                                                Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
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BH251572.1 GI:17138550
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Best Local Similarity 64.3%;
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                  Class: TDNA tagged
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                    61
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
C., Jeske,A., Rarnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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/db_xref="taxon:3702"

/db_xref="taxon:3702"

/dclone="Xalk_04732.39.05.x"

/clone=lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines act of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                            61 GATGCATATACTGCTGAGAGATAACATCACAATTCACAAGCTTCGATGTCACTACAGCCT 120
                                                                         Gaps
                                                                                                                                                                                                    1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTG 60
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                                     DB 17; Length 452;
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
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THEL: 888 538 100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                        Score 42; DB 17; Pred. No. 0.089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.1%; Score 41.8; DB 17;
ilarity 80.3%; Pred. No. 0.099;
Conservative 0; Mismatches 12;
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                                                                     0; Mismatches
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1. .416
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                                   4.18; 57.78;
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Unpublished (2001)
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                                                                       Conservative
                                                                                                                                                                                                                                                     121 ACAGCCATTC 130
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Best Local Similarity
                                                   Best Local Similarity
Matches 75; Conserv
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                                   Query Match
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DEFINITION
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BH749138/c
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KEYWORDS
SOURCE
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29 a 100 c 101 g 124 t 3 others
ын1/2/39 457 bp DNA linear GSS 03-OCT-2001
SALK_006118 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_006118, DNA sequence.
BH172739
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                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots;
Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                         Gadrinab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: eckerésalk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At3g19440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                             Alonso, J. M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Ga., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Zimmerman, J. and Ecker, J. R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
Thould N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Pred. No. 0.12;
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Matches 68; Conserv
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic -	OM nucleic - nucleic search, using sw model
Run on:	December 27, 2002, 23:39:28; Search time 2660 Seconds (without alignments) 11269.132 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-945-376-3 :: 1030 1 cttactatagggcacgcgtgtgtatatatacaaggtctgg 1030
Scoring table	Scoring table: IDENTITY_NUC Gapext 1.0

4109280 Total number of hits satisfying chosen parameters:

2054640 segs, 14551402878 residues

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

em\_fun:\* gb\_ro:\* gb\_sts:\* 9b\_htg: \* 9b\_in: \* 9b\_om: \* 9b\_ov: \* 9b\_pat: \* 9b\_pl: \* gb\_sy:\* gb\_un:\* gb\_vi:\* em\_ba:\* em\_om:\* em\_or:\* em\_in:\* em\_mu:\* em\_ov:\* gb\_ba:\* GenEmbl:\* Database

em\_htg\_inv:\* em\_htg\_other:\* \_htgo\_hum:\* em\_htg\_hum:\* em\_htg\_pln:\* em\_htg\_rod:\* em\_htg\_vrt:\* em\_htg\_mus:\* htg\_mam:\* em\_sts:\* em\_un:\* em\_pat: em\_ph:\* em\_pl:\* em\_ro:\*

is the number of results predicted by chance to have a Pred. No.

em\_htgo\_other:\*

htgo mus:\*

AF14032 Mus muscu AJ289605 Mus muscu AX441981 Sequence 166494 Sequence 166494 Sequence 166399 Mus musculu AF074397 Homo sapi AX098431 Sequence E26792 Novel prote AF237414 Ehrlichia AX320056 Sequence AF077743 Mus muscu AY124482 Danio rer AF051769 Homo sapi AF075270 Hordeum v AL139378 Human DNA AL301655 Human DNA AX320057 Sequence AX320057 Sequence AF153014 Trichomon AX380786 Sequence AB071922 Homo sapi AC025822 Homo sapi U55907 Rattus norv AX253438 Sequence AX253432 Sequence AF429315 Homo sapi AF429315 Homo sapi AL773534 Mus muscu AF457660 Castanea AL773534 Mus muscu AF457660 Castanea AF039526 Homo sapi Continuation (4 of Continuation (3 of AR124194 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES AF114032 MMU289605 PFMAL4P1\_3 PFMAL4P1\_2 AY124482 AX320056 AF077743 AX253431 10 RNU53907 3 AF233737 6 AX253432 AX344560 I66494 MMU63899 AF429315 AF429315 AL773534 AF457660 AF039526 AR124194 AF051769 AF075270 AL139378 HS134N8 AF320057 AF330057 AF30057 AF30786 AF021922 AC025822 AX253428 AX041981 10 10 10 10 6 Query Match Length DB 92633 110000 166703 156325 598 2463 220031 1499 7218 640 1463 125020 11957 682 349980 125020 216878 4400.8 4400.8 4400.9 4400.0 Score 71188 11188 Result Š. ပ O 0000

ALIGNMENTS

AC087887 Homo sapi AC024319 Homo sapi AC105841 Rattus no AL591786 Sinorhizo AL591787 Sinorhizo

AF162890S1 AC087887 AC024319 AC105841

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Castanea

AF162890 Mus muscu

PRI 18-JAN-2002 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 125020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll: Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolis, R.L. AF429315 125020 bp DNA linear P Homo sapiens junctophilin 3 (JPH3) gene, partial cds. AF429315 AF429315.1 GI:17646244 Homo sapiens. Homo sapiens DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 1 AF429315/c LOCUS ORGANISM REFERENCE AUTHORS

944 CGGCATCAGTAGCACCGGCA 963

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NGAKYEGTWSNGLQDGYGTETYSDG"
32731 c 30696 g 28283 t 4254 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="component of the junctional complex between plasma membrane and endoplasmic reticulum"
                                                                                                 1 (bases 1 to 125020)
Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17666 WSYSTSMGYYSSTSCKKYKCSWSSMYKCKTSKSYRRKRSYYWGGGKRAKKKYKZAGRR 17607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17366 RRSMRGSMSSKGWRGYAGRGCYSSSMWSTRKRRSKCYSYKKSYKKGRGKMKGWGGMKRGSK 17307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        704 ACTGCCAACCAGACCTGGCATGGCCTGGTGGCGTCATCTAATTTCTCCTATCAAAGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    884 GCGCAATTGAATTCGAGCCTGATCGAGGTGGTTGGATCGCGCAGGGAAACCTTGAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 CTGCACGAGAGACTCGTTACTGTTC-CGGCCGGAACCGGGACCTCCCTGCTGCTGCTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 764 ACCICCCATIACICCGCCCIGIGCGGCGACCICGIGCCCICGAAITCCACGGGCACACGG
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 Nat. Genet. 29 (4), 377-378 (2001)
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                                                                                                                                                                                                                                                                                                 /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-like 2 (HDL2):
complement(35S81. .35746)
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9.3%; Pred. No. 0.007;
tive 213; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                           complement(<36507. ,>36887)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="junctophilin 3"
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PRI 18-JAN-2002
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1 32731 c 30696 g 28283 t 4254 others
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(Dases 1 to 125020)

Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holmes, S.E., Indersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L. Direct Submission
Submitted (05-0CT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGACGAGACAAATTCGGCATCAACAACCTTTTCGCGCACAAGTAATGTTTGGGTAGGCC 529
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Disease-Like 2 (HDL2)"
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                                                                                                                125020 bp DNA linear P
Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
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complement(<36507. .36887)
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17246 NRRNNRMGKTGCNYMYRRSR 17227
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 216878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22002783.
                           50699 GVHTGVMRWVGYGBCDTHVTYDGGHHGSWGMMKSCGYSDBGKCAKBGSKMCTGSMTKYTC 50758
                                                                                                                                           50818
                                                                                                                                                                                                                    50819 YVKYBSMSVSARKSKGHKVRBSSMKCSRRDMSTSSMWRSMKDRKCSRCSHSHYSKSMGK 50878
                                                                                                                                                                                                                                                                                                               50939 MVDKSRRRNKGSAMRGMKCYCYTSSMRSTKSRSMRWGSKCYYCYGYWSCTKMRSMG 50998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             826 CAGGCACACCACCGCCATCAAAATACGGCCTCTTTGCGGCACGGATCTGCACCGACGGGC 885
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Mus musculus chromosome 2 clone RP23-183012, *** SEQUENCING IN
590 TGTCTCCAACTCTGCATTTTCGGTTCAGAGCAG----TACTGCATTTTGCCATTGTCGCC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGR44; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 21667b bases at least 040 Consensus quality: 216754 bases at least 040 Consensus quality: 216776 bases at least 020 Insert size: 216778; sum-of-contigs Insert size: 216778; sum-of-contigs Insert size: 210770; S.88 error; agarose-fp Quality coverage: 7.01x in 020 bases; sum-of-contigs Quality
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                                                                                             706 TGCCAACCAGACCTGGCATGGCCTGGTGGCGTCATCTAATTTTCTCCTATCAAGAATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL773534.9 GI:22416034
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                        CTCCCATTACTCCGCCCTGTGCGGCGACCTCGTGCCCTCGAATTCCACGGGCACACGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: bM183012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROGRESS ***, 2 unordered pieces.
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AF457660 685 bp DNA linear PLN 13-JAN-2002 Castanea dentata clone ACS2 vascular protein gene, promoter region.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fagales; Fagaceae; Castanea.
1 (bases 1 to 685)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 137585 ATTTGCATTTGATGAACTGTCTTTATTTTAAATGATTAGAAATAGTACATTTAAAAGGA 137644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 137525 AATTGTCTAAAATAAGCAAAATTTACAAGATTGACTATATACTTCCCTCTGTATTTAGTT 137584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 137645 CTTATCATATTGTCTCTCTTTATATTACTAAGATATCATTAATTTAATTTTCAATCCCAGCCA 137704
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Cloning and characterization of promoters from American chestnut
capable of directing reporter gene expression in transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 ATTITITATCICCCCAACCGGCATTAGTAAGCAGGCCCCCAACGCATTCAAATTCGATGTA 296
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                                           15292 15391: gap of 100 bp 115392 216878: contig of 201487 bp in length. Location/Qualifiers 1. 216878
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44.4; DB 2; Length 2
Pred. No. 0.31;
0; Mismatches 146; Indels
                    15291: contig of 15291 bp in length
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                                                                                                                              1. .216878
/organism="Mus musculus"
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/chromosome="2"
/clone="RP23-183012"
/clone=lib="RPC1-23"
1. .15291
/note="assembly_fragment:02090
fragment_chain:1"
15392. .216818
/note="assembly_fragment:03034
fragment_chain:1"
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Connors, B.J., Maynard, C.A. and Powell, W.A.
Direct Submission
Submitted (12-DEC-2001) EFB, SUNY-ESF, 1 F/
NY 13210-2788, USA
Location/Qualifiers
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/db_xref="taxon:134033"
/clone="ACS2"
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AF457660.1 GI:18140057
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Unpublished
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Matches 132; Conservative
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be preserved.
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PAT 16-MAY-2001

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3 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTCTGAA
                                                                          AR124194 6078 bp
Sequence 1 from patent US 6171857.
AR124194 GI:14109555
                                                                                                                                                                                 Unclassified.
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PFMAL4P1_3
Continuation (4 of
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Best Local §
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Homo sapiens MHC class I related protein 1 (MR1) gene, partial cds.
AF039526
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                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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Riegert, P., Wanner, V. and Bahram, S.
Genomics, isoforms, expression, and phylogeny of the MHC class
I-related MR1 gene
J. Immunol. 161 (8), 4066-4077 (1998)
                                                                                                        Gaps
                                                                                                                                1 CTTACTATAGGGCACGCGTGGTCGACGCCCGGGCTGGTATGAAGGTGGGAACCTCACTG 60
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1423)
Riegert, P., Wanner, V., Hauptmann, G. and Bahram, S.
Direct Submission
Submitted (22-DEC-1997) EG, Basel Institute for Immunology,
Grenzacherstrasse 487, Basel 4005, Switzerland
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.47;
0; Mismatches 1; Indels 0
                                                                          Length 685;
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/note="contains putative promoter and 5/UTR"
<1390. >14423
/gene="MRI"
                                                                                                    37; Indels
1. .685
/note="vascular protein promoter region"
126 c 117 g 189 t
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/evidence=not_experimental
1390 . >1423
/gene="MRI"
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/evidence=not_experimental
/product="MHC class I related
/protein_id="AAD0172.1"
/db_xref="GI:4104808"
                                                                       Score 42.8; DB Pred. No. 0.31; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGELMAFLLPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 1423
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                       AF039526.1 GI:4104807
                                                                       ch 4.2%;
1 Similarity 63.7%;
65; Conservative
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97.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="MR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="1q25"
1. .>1423
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Best Local Similarity 97.78
Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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 misc_feature
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AUTHORS
TITLE
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MEDLINE
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AUTHORS
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                                                                                                                                                                                                                                                                RESULT 5
AF039526
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44

1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTAGAA

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from base 300001 (ALO34557 Plasmodium falciparum 3D
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                                Leucine zipper protein, KARP-1 and methods of regulating DNA dependent protein kinase activity Patent: 18 6171877-A 1 09-JAN-2001; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                LOCUS PFMAL4P1 Accession AL034557
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4.1%; Score 41.8; DB 2; Length 92633;
Best Local Similarity 65.6%; Pred. No. 1.6;
Matches 61; Conservative 0; Mismatches 32; Indels 0;
                                                                                                                                                                                          Length 6078;
                                                                                                                                        36 others
                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                            9 CTTACTATAGGGCACGCGTCGACGGCCCGGCTCGAA 52
                                                                                                                                                                                                                                                          1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAA
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Pred. No. 0.62;
0; Mismatches
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Pred. No. 1.6;
0; Mismatches
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210000
310000
392633
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210000
310000
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PFWAL4P1_3 300001
Continuation (3 of 4) of PFWAL4P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence split into 4 fragments
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ilarity 97.7%;
Conservative
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Best Local Similarity 65.6%;
Matches 61; Conservative
1 (bases 1 to 6078)
Hendrickson, E.A.
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200001
300001
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AF075270 1094 bp DNA linear PLN 24-SEP-1998 Hordeum vulgare high affinity sulfate transporter (HVST1) gene, promoter region, 5'UTR, and partial cds. AF075270. GI:3643823
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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Spermatophyta; Viridiphyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Hordeum.

1 (bases I to 1094)

Vidmar,J.J., Schjoerring,J.K., Touraine,B. and Glass,A.M.D.

Regulation of the HVSTI gene encoding a high affinity sulfate
                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 1094)
2 (bases 1 to 1094)
2 (bases 2 to 1094)
2 (bases 3 to 1094)
2 (bases 3 to 1094)
3 (bases 4 to 1098)
5 (bases 4 to 1098)
5 (bases 5 to 1098)
6 (bases 5 to 1098)
6 (bases 6 to 1098)
6 (bases 7 to 
                                                                                                                           1 (bases 1 to 11957)
Csoka, A.B., Scherer, S.W. and Stern, R.
Expression analysis of six paralogous human hyaluronidase genes clustered on chromosomes 3p21 and 7q31
Genomics 60 (3), 356-361 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hyaluronidase-like pseudogene 1; exon/intron structure not yet determined"
                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (28-FEB-1998) Pathology, University of California,
Parnassus St. at 3rd Ave, San Francisco, CA 94143, USA
Location/Qualifiers
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100.0%; Pred. No. 1.8;
tive 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
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<1. .>11957
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1025. .>1094
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                                                                                                                                                                                                                                                                                                             2 (bases 1 to 11957)
Csoka, T.B.
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                                                      Homo sapiens
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LOCUS
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KEYWORDS
SOURCE
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Du,S., Gao,J. and Anyangwe,V.
Direct Submission
Submitted (20-JUN-2002) Center of Marine Biotechnology, University
of Maryland Biotechnology Institute, 701 E. Pratt St, Baltimore, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /traislation="MELETNPYFFNDQRFYEGADNFFQSRINGGFEGAGYODRNSMM GLCGGGRMLTTTVGLEDKPSPSSSLGLSMSPHOEOGHCPGGCLPWACKVCKRKSVTMD GLCGGGRMLTTTVGLEDKPSPSSSLGLSMSPHOEOGHCPGGCLPWACKVCKRKSVTMD NGVRATLREKRLKKVNEAFPELKRSTLMNPNORLEKVEILKSAIQYISKLVSLUNQOBHEOGNILHYRATAAAPHTGVSSSSDGGGSTCGSSPEWSSASDHCVPAYSSAHED LLNDDSSEQSNLRSLTSIVDSITGTEATPVAYSVDISK"
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Homo sapiens hyaluronidase-like pseudogene l (HYALP1), partial
                                                                                                                                                                                                                                                                    VRT 31-JUL-2002
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 4260)
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Du,S., Gao,J. and Anyangwe,V.
Muscle-specific expression of myogenin in zebrafish embryos
controlled by multiple regulatory elements in the promoter
unpublished
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join(652. .1309,2288. .2393,3002. .3599)
/product_"myogenin"
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Pred. No. 1.5;
                                                                                                                             Db 107255 TTTCCATATTTTAAAAAGGCTCATATAATAAT 107223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="myogenin"
/protein_id="AAM82616.1"
/db_xref="GI:22035405"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .4260
/organism="Danio rerio"
/db_xref="taxon:7955"
                                                                            GATGCATATACTGCTGAGAGATAACATCACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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3002. .3599
/number=3
a 797 c
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/number=1
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AUTHORS
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/translation="messsalukrpnDerpderesgisQallelemnsDlkaQlreln
ITAAKEIELGGGRRAIIIFVPIPQLKSFQKIQVRLVRELEKRFSGKHVVFIVQRRILD
KPTRKSRTKNKQRRPRSHTLTAVHDAILEDLVFPSEIVGKRIRVKLDGSRLIKVHLDK
AQQNNVEHKVETFSGVYKKLTGKDVNFEFPEFQLQTKMTT"
complement(1098 .11260)
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match: proteins: Tr:092NS1 Sw:040101 Sw:043105 Tr:09VA91
Tr:023312 Sw:P02362 Sw:P73821 Sw:P48155 Sw:P33514
Tr:029190 Tr:013167 Sw:P50894"
                                                                                                                                                                                                                                                                                                                                                                                                      2621. .2932
/hote="MLTIC repeat: matches 147. .466 of consensus"
2933. .3198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4184. 4319
/note="L2 repeat: matches 2609. .2748 of consensus"
/note="L2 repeat: matches 1807. .2082 of consensus"
/note="L2 repeat: matches 1807. .2082 of consensus"
5016. .5305
                                                                                                                                                                                       163. .580
/note="MER5A repeat: matches 17. .138 of consensus"
                                                                                                                                                                                                                                                                                                                                  1320. .2372
'note="L2 repeat: matches 2700. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
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/db_xref="G1:11544936"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9516. .9818
/note="Aluy repeat: matches 1. .303 of consensus"
10023. .10311
/note="Aluy repeat: matches 1. .293 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(10938..11116)
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complement(10938..11050)
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/gene="bA27185.1"
                                                                                                                                                                                                                                                                                   /note="AluJb repeat: matches 1. 2320, .2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5016. .5305
/note="Alusx repeat: matches 1.
5493. .5804
                                                                                                                                                                                                                    1191. .1400
/note="MER3 repeat: matches 1.
1669. .1922
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110997. .11430
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                                              /db_xref="taxon:9606"
                                                                                          /clone="RP11-271B5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, Calonited (18-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
On Jun 4, 2000 this sequence version replaced gi:8246895.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RPD1-271B5 is from the library RPOI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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Human DNA sequence from clone RP11-271B5 on chromosome 13 Contains a gene for a protein similar to ribosomal protein S7, the FGF9 (fibroblast growth factor 9 (glia-activating factor)) gene, ESTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166703)
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                     high affinity sulfate transporter"
                                                                                                                                                         /product="high affinity sulfate transporter"
/protein_id="AAC42664.1"
/db_xref="GI:3643824"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STSs, GSSs and CpG islands, complete sequence. AL139378
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llarity 95.5%; Pred. No. 1.3;
Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                              /translation="MP'
                                                             /gene="HVST1"
1090, .>1094
/gene="HVST1"
/codon_start=1
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'dene="HVST1"
                                           .1089
                   /product="h
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JOURNAL
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COMMENT

FEATURES

.288 of consensus"

.294 of consensus"

.209 of consensus"

ORIGIN

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/note="LiM4c repeat: matches 1260. .1464 of consensus"
15515. .15827
/note="AluY repeat: matches 1. .303 of consensus"
/note="14 copies 3 mer tta 78% conserved"
16651. .16946
/note="Alu8 repeat: matches 1. .296 of consensus"
//note="Alu8 repeat: matches 1. .296 of consensus"
//1742. .17709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .6145 of consensus"
                                                                                                                                                                                                                                                                      12941. .13266
/note="WER2 repeat: matches 1. .345 of consensus"
13779. .13989
.1344c repeat: matches 1511. .1736 of consensus"
14084. .14294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18944. .19037 / Octe="MIR repeat: matches 49. .143 of consensus" 19023. .19447 / Octe="match: GSS: Em:AQ630744" | Octe="match: GSS: Em:AQ630744" | Octe="match: GSS: Em:AQ630723" | Octe="match: GSS: Em:AG630723" | Octe="match: GSS: 
                                                                                                                                                                                             11884. 12154
/note="LiM4 repeat: matches 2891. .3182 of consensus"
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31396. .31605
/note="MLT2G repeat: matches 228. .386 of consensus"
31899. .32195
/note="Alux repeat: matches 1. .297 of consensus"
32459. .32670
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//note="MLT2F repeat: matches 121. .349 of consensus" 33068. .33143
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/note="MRR5B repeat: matches 6. .177 of consensus" 29406. .29491
/note="MRR5A repeat: matches 74. .159 of consensus" 29902. .30303
/note="LiPA5 repeat: matches 5740. .6145 of consensus"
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/note="MLT2CB repeat: matches 1. .494 of consensus"
26705. .27376
/note="match: GSS: Em:AQ379984"
26925. .27220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Alusg repeat: matches 1. .296 of consensus" 742. .17709
'note="Alusx repeat: matches 6. .269 of consensus"
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/note="Alux repeat: matches 1. .303 of consensus"
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                                                                                                                                                                    matches 3.
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28519. .28685
/note="match: GSS: Em:AQ559377"
                                                                                           note="match: GSS: Em:AQ554409"
11672. .11854
note="MER5A repeat: matches 3.
                         'note="match: GSS: Em:AQ264373"
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Direct Submission

Lirect Submission

Libract 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS134N8 110-MAR-2001
Human DNA sequence from clone RP1-134N8 on chromosome 20p12.
Contains STSs, GSSs and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           ó:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156325)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48869 TACAATATTTTAAAATATTTTTTAAAGCTATAATAATTAGAACAGTGTCATATGAATTAT 48810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422
                                                                                                                                                                                                                                                                                                                                                                                                                                    303 TACTICATITIGGIICAGAIIIGAACGAIGICAGIIITCAAICCACAIGCAACAGAAICCG 362
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                               Length 166703;
/note="19 copies 4 mer ctct 65% conserved" 33069 .33140 /note="36 copies 2 mer tc 65% conserved" 33401 .33472 4 mer atat 81% conserved" 33402. .33473
                                                                                                                                                                                                                                                                                                                                                           67; Indels
                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                          Score 40.8; DB; Pred. No. 3.5; 0; Mismatches
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HTG; CpG island.
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Best Local Similarity 54.7%;
Matches 81; Conservative
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FEATURES

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12921. 13046
// Acce="FLIAM_A repeat: matches 1. 127 of consensus"
14487. 14958
// Acce="L2 repeat: matches 2225. 2749 of consensus"
15346. 15405
// Acce="3" copies 20 mer 86% conserved"
15357. 15404
// Acce="2" copies 2 mer ca 95% conserved"
15562. 15708
// Acce="2" copies 2 mer ca 95% conserved"
15662. 15708
// Acce="2" consensus"
15602. 15708
// Acce="2" consensus"
15602. 15708
// Acce="2" consensus"
15804. 16914
// Acce="2" consensus"
16814. 16400
                                                                                                                                                                                                                                                                                                                                                                                                       .1368 of consensus"
                                                                                                                                                                                                                                                                                                                                          4422 . 4603
/note="HAL1 repeat: matches 579. .771 of consensus"
4847. .4897
/note="liMEc repeat: matches 1318. .1368 of consensi
                                                                                                                                                                                                                                                                                                                                                                                                                    4904. :5263
/note="TIK18A repeat: matches 1. :603 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7290. .7597
/note="AluSx repeat: matches 1. .312 of consensus"
8305. .8851
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                                                                                                                                                of consensus'
                                                                                                                                                           1278. .1446
/note="WER3 repeat: matches 1. .171 of consensus"
1686. .1846
/note="MIR repeat: matches 29. .179 of consensus"
2396. .2495
/note="5_copies 20 mer 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17529. 17978
/note="match: GSS: Em:AQ231626"
17852. 18269
/note="MSTB repeat: matches 2. .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         5275. :5520
/note="123 copies 2 mer tt 54% conserved"
6040. :6834
                                                                                                                                                                                                                                                     note="5 copies 20 mer 75% conserved"
2400. 2485
note="43 copies 2 mer ta 77% conserved"
                                                                                                                                                .136
                                                                                                                                                                                                                                                                                                            3504, 3563
/note="3_copies 20 mer 90% conserved"
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                                                                                                    /clone_11b="RPCI-1"
1145. 1261
/note="MER5A repeat: matches 9.
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8318. .8819
/note="match: GSS: Em:AQ228387"

    156325
    /organism="Homo sapiens"
/db_xref="taxon:9606"
    /chromosome="20"

                                                                      /map="p12"
/clone="RP1-134N8"
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Complement(3036. 30597)

Anote="match: STS: Em:624652"
13036. 30760

Anote="MLT11 repeat: matches 92. 385 of consensus"
30812. 31214

Anote="MLT21 repeat: matches 5266. 5711 of consensus"
10012. 31219. 31280

Anote="LIME repeat: matches 5266. 5711 of consensus"
11219. 31300

Anote="11ME repeat: matches 4988. 5266 of consensus"
1301. 3150.
13150. 31677

Anote="11ME repeat: matches 4430. 4548 of consensus"
15162. 31677

Anote="11ME repeat: matches 274. 671 of consensus"
15162. 31677

Anote="match: 635: Em:Aq636331"

Anote="match: 635: Em:Aq636331"
                                                                                                                                                                                                                                                                                                  32820. 33283.

// note="17 copies 2 mer tg 85% conserved"
33824. 33231
// note="19 copies 2 mer tg 84% conserved"
33987. 34525
// note="7 copies 77 mer 95% conserved"
// note="7 copies 77 mer 95% conserved"
// note="match: GSS: Em:AQ540824"
// note="match: GSS: Em:AQ540824"
// note="Match: GSS: Em:AQ366937"
// note="MIR repeat: matches 21. .262 of consensus"
// note="Alux repeat: matches 1. .311 of consensus"
// note="Alux repeat: matches 1. .311 of consensus"
// note="Alux repeat: matches 1. .254 of consensus"
// note="Alux repeat: matches 1. .254 of consensus"
// note="Alux repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 159. .227 of consensus'
//note="Militaria repeat: matches 92. .142 of consensus" 21187. .21455 //note="Alus repeat: matches 1. .275 of consensus" complement(21429. .21869) //note="match: GSS: Em:AQ033647" //note="match: GSS: Em:AQ033647" //note="match: GSS: Em:AQ528323" //note="match: GS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .308 of consensus"
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25002. .25244
/note="L2 repeat: matches 2454. .2
26228. .26594
/note="THELC repeat: matches 1. .3
complement(26328. .26717)
/note="match: GSS: Em:AQ084144"
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32750. .33158
/note="match: GSS: Em:AZ032717"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                Db 151345 TARATARATGGTARAACTATARAATATCTARGAAATGTATCTCTTTTCAGGTTTTTCAGGAA 151404
                                                                                                                                                                                                                                            Db 151285 AGTTTTATTTTAAATAAACATATTTTAATGTATGAAATTTGCTAATTTAAAGAAAAATCT 151344
                                                                                                                                                                                                                                                                              395 GCAACAGAAGTTAAAACCATAAACATCCAATTAACGAGTTGCATTTTAGATCTTTTAGAGA 454
                                                                                                                                                                                                            335 AGTITCAATCCACATGCAACAGAATCCGCAGAAGAATTCATCCAATTCACACATAAAGCA 394
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                                                                                                                                                                              Gaps
 /note="L2 repeat: matches 2577. .2710 of consensus" 39012. .39140
/note="MLT1H repeat: matches 339. .541 of consensus" complement(40115. .40665)
/note="match: GSS: Em:AQ424883"
/note="large at: matches 2605. .2750 of consensus" note="L2 repeat: matches 2605. .2750 of consensus"
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Polyncleotide sequences from rice
Patent: WO 0181606-A 14 01-NOV-2001;
Akkadix Corporation (US)
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Sequence 14 from Patent W00181606.
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AX320057.1 GI:17901561
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/organism="Oryza sativa"
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a 131 c 113 g 179
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VALFKVLEYTKYEKPGEYGDPKHETIYVDVKKKVFNQDPKIQEYCKTLEVGKKYRVCY
1 (bases 1 to 1463)
Crouch,M.V. and Alderete,J.F.
Trichomonas vaginalis has two fibronectin-like iron-regulated genes
Arch. Med. Res. 32 (2), 102-107 (2001)
21242390
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                                                                                                                                     2 (bases 1 to 1463)
Crouch,M.-L. and Alderete,J.F.
Direct Submission
Submitted (19-MAY-1999) Microbiology, UTHSCSA, 7703 Floyd Curl Dr,
San Antonio, TX 78284-7758, USA
Location/Qualifiers
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796. .1173
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; Search time 55 Seconds
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5743.219 Million cell updates/sec
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1 cttactatagggcacgcgtg......tgtatatatacaaggtctgg 1030
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                           December 27, 2002, 20:39:18
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Issued\_Patents\_NA:\*

Database

## sequence 14, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 11, Appli Sequence 14, Appli Sequence 28, Appli Sequence 18, Appli Sequence 19, Appli Sequence 19, Appli Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli Sequence 11, Appli Sequence 31, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6 Description US-09-424-283-6 US-08-223-463-14 US-09-233-1463-14 US-09-474-283-7 US-09-577-648-4 US-09-577-648-4 US-09-276-599-13 US-09-276-599-13 US-09-276-599-13 US-09-276-599-13 US-09-276-599-13 US-09-276-598-14-28 US-09-545-814-15 US-09-545-814-13 US-09-545-814-13 SUMMARIES Query Match Length DB 39..8 39..8 39..8 38..4 38.4 Score Result ٠ يو

137, Appl 1688, Ap 1688, Ap 53, Appl 4, Appli 6, Appli 1291, Ap 121, Appl 17, Appl 18, Appl 19, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 12, Appl 12, Appl 13, Appl 14, Appl 16, Appl 17, Appl 18, Appl 18, Appl 19, Appl 19, Appl 19, Appl 19, Appl 10, Appl 11, Appl 1	
	6078;
US-09-247-155-37 Sequence US-09-144-001C-1688 Sequence US-09-134-001C-1688 Sequence US-08-565-300A-4 Sequence US-08-566-300A-5 Sequence US-08-566-300A-5 Sequence US-08-566-300A-5 Sequence US-08-566-300A-5 Sequence US-08-596-300A-5 Sequence US-08-596-300A-3 Sequence US-08-596-300A-5 Sequence US-09-503-195A-4 Sequence US-08-731-195A-4 Sequence US-08-731-195A-20 Sequence US-08-74-394A-20 Sequence US-08-74-394A-20 Sequence US-08-74-394A-21 Sequence US-08-74-39	Score 42.4; DB 4; Length Pred. No. 0.0041; 0; Mismatches 1; Indels GACGGCCGGGCTGGTATGAA 44 
36 3.5 555 4 37 3.4 189 4 47 2 4.8 3.4 47 2 4.8 3.4 1881 2 4.8 3.4 3748 2 4.8 3.4 3796 2 3.3 3.1 376 4 3.3 3.1 1218 3 1.4 3.0 246240 2 1.4 3.0 246240 2 1.4 3.0 246240 2 1.4 3.0 246240 2 1.4 3.0 246240 2 1.4 3.0 246240 2 1.1 4 3.0 246240 2 1.1 4 3.0 246240 2 1.1 4 3.0 246240 2 1.1 8 3.1 1218 3 1.1 8 3.1 1218 3 1.1 8 3.1 1218 3 1.1 8 3.1 1218 3 1.1 8 3.1 1218 3 1.1 8 3.0 1246240 2 1.1	: (232)(232) : (234)(234) : unsure : (453)(453) : unsure : (473)(473) : unsure : (610)(610) : unsure : (610)(612) : (1014)(1014) : unsure : (1014)(1014) : unsu
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PatentIn Ver. 2.0
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APPLICANT: Cairney, John
APPLICANT: Perrera, Ranjan
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Best Local Similarity 89.49
Matches 42; Conservative
                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                           ; CLONE: pTZgpt-F1s
US-08-232-463-14
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ORGANISM: Pinus taeda
                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39.8; DB 4;
Pred. No. 0.021;
0; Mismatches 2;
                                                                                                    APPLICANT: Grimes, et al.
TITLE OF INVENTION: Sucrose binding proteins
FILE REFERENCE: 4630-50206
CURRENT APPLICATION NUMBER: US/09/424,283
CURRENT FILING DATE: 1999-11-19
FRIOR PELLING DATE: 1999-11-19
FRIOR APPLICATION NUMBER: PCT/US98/10465
FRIOR APPLICATION NUMBER: D6.221
FRIOR FILING DATE: 1998-05-21
FRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 3718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHETELINDER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30472/114 IMMU
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1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: EP 91 114 300.6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                  Sequence 6, Application US/09424283
Patent No. 6437219
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-AUG-1991
ATORNEY/AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.9%;
Best Local Similarity 95.3%;
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Glycine max US-09-424-283-6
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22313-0299
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COUNTRY:
                                  US-09-424-283-6
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                                                                                                                        561 TGGCACCCGATGGATGTCCCATCCGAACTTGTCTCCAACTCTGCATTTTCGGTTCAGAGC 620
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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  Length 7218;
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                                           Indels
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Query Match 3.8%; Score 39.6; DB 1; Best Local Similarity 5.0%; Pred. No. 0.035; Matches 15; Conservative 163; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09424283
Patent No. 6437219
GENERAL INFORMATION:
APPLICAMY: Grimes, et al.
TITLE OF INVENTION: Sucrose binding proteins
FILE REFERENCE: 4630-56206
CURRENT APPLICATION NUMBER: US/09/424,283
CURRENT FILING DATE: 1999-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.8%; Score 39; DB
89.4%; Pred. No. 0.01
Live 0; Mismatches
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CORRENT APPLICATION NUMBER: US/09/323,195A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 19
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US-09-323-195A-5; Sequence 5, Application US/09323195A; Patent No. 6462257; GENERAL INFORMATION:
                                                            42; Conservative
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US-09-276-599-13
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                                 Best Local Similarity
Matches 42; Conserv
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Matches 38; Conserv
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US-09-276-599-14/c
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US-09-276-599-13/C
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LENGTH: 763
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                    Query Match
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APPLICANT: Gorczynski, Reginald M.
APPLICANT: Gorczynski, Reginald M.
TITLE OF INVENTION: Methods and Compositions for Immunomodulation
FILE REFERENCE: 9579-21
CURRENT FILING DATE: 2000-05-05
PRIOR PAPLICATION NUMBER: US 60/064,764
PRIOR PALING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2791
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0.042;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                       2 TTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTA 40
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APPLICANT: Lappegard, Kathryn
APPLICANT: Lappegard, Kathryn
APPLICANT: Martino-Catt, Susan
TITLE OF INVENTION: Seed-Preferred Promoters
FILE REFERENCE: 0869
CURRENT APPLICATION NUMBER: US/09/377,648
CURRENT APPLICATION NUMBER: US/097,233
EARLIER APPLICATION NUMBER: US 60/097,233
EARLIER FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 921
                                                                                                                                                                                                                                        3.8%; Score 39; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US98/10465
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: US 60/047,568
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-570-367C-1; Sequence 1, Application US/09570367C; Patent No. 6338851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/09377648
; Patent No. 6225529
                                                                                                                                                                                                                                        Query Match 3.8%
Best Local Similarity 100.0
Matches 39; Conservative
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; ORGANISM: Mus musculus
US-09-570-367C-1
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; LOCATION: (1)...(922)
US-09-377-648-4
                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Glycine max
US-09-424-283-7
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ORGANISM: Zea mays
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US-09-377-648-4/c
                                                                                                                                           LENGTH: 4526
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3.7%; Score 38.4; DB 4; Length 2791;
87.5%; Pred. No. 0.051;
Live 0; Mismatches 6; Indels 0
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                                                                                                                      4 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09276599;
Patent No. 6380459;
GENERAL INFORMATION:
APPLICANT: Perera, J. Ranjan
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Composition and methods for the
TITLE OF INVENTION: Modification of gene expression
FILE REFERENCE: 11000.1036
CURRENT APPLICATION NUMBER: US/09/276,599
CURRENT FILING DATE: 1999-03-25;
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Perera, J. Ranjan
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Composition and methods for the
TITLE OF INVENTION: Modification of gene expression
FILE REFERENCE: 11000.1036
CURRENT APPLICATION NUMBER: US/09/276,599
CURRENT FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
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3. 0.034;
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Patent No. 6380459
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Nishi, Kazunori
                                                                                                                                Boston,
                                                                                                                                                          USA
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US-09-570-367C-1/C
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                                                                                                                                                          COUNTRY:
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                      APPLICANT: Perrera, Ranjan
TITLE OF INVENTION: VICILIN-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND
TITLE OF INVENTION: METHODS OF USING THE SAME
FILE REFERENCE: IPST0009
CURRENT APPLICATION NUMBER: US/09/323,195A
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Pred. No. 0.065;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                   4; Length 565;
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Pred. No. 0.033;
0; Mismatches 2; Indels
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Patent No. 6235878
GENERAL INFORMATION:
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Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                    PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.13
Matches 39; Conservative
 Pullman, Gerald
                                                                                                                                                                                              OTHER INFORMATION: n at 46 OTHER INFORMATION: n at 50 OTHER INFORMATION: n at 50 OTHER INFORMATION: n at 50 OTHER INFORMATION: n at 54 OTHER INFORMATION: n at 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), NAME/KEY: CDS
; LOCATION: (119)..(1588)
US-09-424-283-5
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                                                                                                                                                                        ORGANISM: Pinus taeda
                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
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US-08-913-014A-18
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                                                                                                                                SEQ ID NO 5
LENGTH: 565
                                                                                                                                                            TYPE: DNA
 APPLICANT:
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APPLICANT: GOTCZYNSKI, Reginald M.
APPLICANT: GOTCZYNSKI, Reginald M.
TITLE OF INVENTION: Methods and Compositions for Immunomodulation
FILE REFERENCE: 9579-21
CURRENT APPLICATION NUMBER: US/09/570,367C
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1997-11-07
NUMBER OF SEQ ID NOS: 22
SOFWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.4; DB 4; Length 48;
Pred. No. 0.012;
0; Mismatches 1; Indels
APPLICANT: HIXIGHI, TUKIKO
APPLICANT: Shintani, Yasushi
TITLE OF INVENTION: NOVEL FAS LIGAND-LIKE PROTEIN, ITS
TITLE OF INVENTION: PRODUCTION AND USE
NUMBER OF SEQUENCES: 25
CORRESPEDIBENCE ADDRESS:
ADDRESSE: David G. Conlin, Esq.
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & USHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 CICACTATAGGGCACGCGTCGACGACGGCCCGGGCTGGT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGT 39
                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,014A
FILING DATE: 04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP97/02480
FILING DATE: J11y 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG G. CONLIN
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342/47694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09570367C; Patent No. 6338851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.68;
97.48;
                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.4
Matches 38; Conservative
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TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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LENGIH: 1478
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                                                                                                                                                       Sequence 28, Application US/09545814

Batent No. 6416977

GENERAL INFORMATION:
APPLICANT: Becher, Anna M.

TITLE OF INVENTION: FLEA CHITINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: USS THEREOF
FILE REFERENCE: FC-5-C1

CURRENT APPLICATION NUMBER: US/09/545,814

CURRENT APPLICATION NUMBER: US/09/545,814

PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Becher, Anna M.

TITLE OF INVENTION: FLEA CHTINASE NUCLEIC ACID MOLECULES, PROTEINS AND TITLE OF INVENTION: USES THEREOF TITLE OF INVENTION: USES THEREOF CURRENT PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 CATTCCGAGCAGGGCGCTTAGGACGGCCGTCAATAACTTGGAGGAACTGCCAAGAATGTG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 ATATACTGCTGAGAGATAACATCACAATTCACAAGCTTCGATGTCACTACAGCCTACAGC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 GAAAGCCCTTCGCAATTCTTGGACAAAGTATAAAAATTTGTCTTTGTCGGAAAAACTGCC 277
                Gaps
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                Indels
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                                                                 2791 ACTATAGGCCACGCGTGGTCGACGCCCGGGCTGGTCTG 2753
                ;
                                              42
                                                4 ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATG
 No. 0.11;
                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Tagged Ctenocephalides felis
   Pred.
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ilarity 97.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 40 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1467)
US-09-545-814-28
 Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; GENERAL INFORMATION:
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US-09-545-814-28/c
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Best Local Simi
Matches 114;
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                                                                                                                                                             66 ATATACTGCTGAGAGATAACATCACAATTCACAAGCTTCGATGTCACTACAGCCTACAGC 125
                                                                                                                                                                                                                                                 126 CATTCCGAGCAGGCGCTTAGGACGCCGTCAATAACTTGGAGGAACTGCCAAGAATGTG 185
                                                                                                                                                                                                                                                                                                                                                                                                                   246 TCCCCAACCGGCATTAGTAAGCAGGCCCCCAACGCATTCAAATTCGATGTAATTGTCTAC 305
                                                                                                                                                                                                                                                                                                                                    186 GATTACAACAGTTCTATCTGAGCGACAGTCTAAACGCAGCTTTGTATAGTCATTTTTATC
                                                                                                                        ö
                                                                                 Length 1478;
                                                                                                                        Indels
                                                                              Score 37.2; DB 4;
Pred. No. 0.087;
0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 28, 2002, 00:01:55 Job time: 63 secs
TYPE: DNA CLENOCEPhalides felis US-09-545-814-30
                                                                              Query Match 3.6%;
Best Local Similarity 47.1%;
Matches 114; Conservative
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SALK\_0469 SALK\_0180 SALK\_0103

BH214178

BH212774 BH749138 BH172739 BH251074

Drosophil SALK 0002 SALK 0108 SALK 0108 SALK 0109 SALK 0109 SALK 0109 SALK 0109 SALK 0328 SALK 0328 SALK 0341 SALK 0341 SALK 0031 SALK 0045 SALK 0045 SALK 0109 SALK 0165 SALK 0165

Scoring table:

Total number

Database

Searched:

Perfect score:

ritle:

Sequence:

OM nucleic

Run on:

BH253202 BH612446 BH612446 BH612500 BH613739 BH617395 BH177395 BH17795 BH17795 BH17795 BH25426 BH25426 BH25421 BH177334 BH177334

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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 388)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Rarnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH747511
SALK_018023.45.85.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK_018023.45.85.x, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis Genome
Unpublished (2001)
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
TH: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                 BH170645
BH25106
BH254020
BH254020
BH171573
BH171573
BH170269
BH170269
BH170269
BH170269
BH17099
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BH212774
BH749138
BH172739
BH251074
BH253202
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BH172612
BH250920
BH251621
               BH610787
BH214178
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BH188842
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BH747511.1 GI:18960626
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sequence.
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 42.6
42.2
42.2
42.2
42.2
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BH747511/c
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AUTHORS
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
 LOCUS
                                                                     BH747511 SALK_0180
BH251364 SALK_0114
BH6177520 SALK_0372
BH613783 SALK_0349
BH250931 SALK_0107
BH634101 SALK_0447
                                                                                                                                   (without alignments)
8493.560 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                   cttactatagggcacgcgtg......tgtatatatacaaggtctgg 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                December 28, 2002, 00:00:48; search time 1964 Seconds
                                                                                                                                                                                                                                                                                                                                     32308132
                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BH251364
BH617520
BH613783
BH250931

    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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em_gss_other:*
em_gss_pro:*
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em_estlu:*
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em_htc:*
gb_estl:*
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gb_estl:*
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gb_estl:*
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em_gss_lun:*
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Maximum DB seq length: 200000000
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469
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST:*
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SALK\_0036 SALK\_0297 SALK\_0297 SALK\_0135 SALK\_0135 SALK\_0123 036\_P=10-T3 end of SALK\_0105 SALK\_0105

BH611714 BH251902 BH188842

BH752369 BH170998 BH611050 BH611042 AL625781 BH172612 BH250920 BH251621

27-FEB-2002 lines DNA

43.6 43.4 42.8 42.8

4 2 2 4 5 9

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Score

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Mon Dec 30 17:32:54 2002

us-09-945-376-3.rst

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BH251364 469 bp DNA linear GSS 28-NOV-2001 SALK_011461 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_011461, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Furbidopsis thaliana
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 469)
Alonso,J.W., Leissey,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
                                                                                                                                                                                      /db_xref="taxon:3702"
/Clone="SALK_018023.45.85.x"
/Clone="Taxabioopsis thaliana TDNA insertion lines"
/Cotone_lib="Arabioopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 95 c 82 g 110 t 3 others
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3959400 Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTG 60
                of
                end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4%; Score 45; DB 17; Length 388; 78.3%; Pred. No. 0.0094;
TDNA. This sequence lies within 300 bases of the 3' At1957820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/strain="Columbia 0"
/bxref="taxon:3702"
/clone="SalK_011461"
                                                                                                                                              /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                      Location/Qualifiers
1. .388
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                                                             Class: TDNA tagged
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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/clone="SALK_037200"
/clone="Taxon:3700"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
insertion. Details of the protocols used car
http://signal.salk.edu/tdna_protocols.html"
81 g 135 t 40 others
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                                                                                                                   Score 43.6; DB 17; Length 469;
Pred. No. 0.028;
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
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be found at
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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A Sequence-Indeed Library of Insertion Mutations in the Arabidopsis Genome
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 888 453 4100 x1752
                                                                                                                                                                                             Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379
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Best Local Similarity 75.7%; Pred. No. 0.046;
Matches 53; Conservative 0; Mismatches 17;
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/organism="Arabidopsis thaliana"
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/strain="Columbia 0"
/db.zref="taxon:3702"
/dlone="SALK_034950"
/clone="SALK_034950"
/clone="Taxon:37050"
/clone="Taxon:37050"
/clone="Taxon:37050"
/clone="Taxon:37050"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/note="Taxon:37050"
/clone="Ib="Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
34 a 31 c 31 g 28 t
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                                                       SALK_034950 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_034950, DNA sequence.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alonso, J.M., Leissé, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeska, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 0.029;
0; Mismatches 37;
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Location/Qualifiers
1. 124
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Similarity 63.7%;
55; Conservative 0
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Arabidopsis thaliana
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Unpublished (2001)
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BH613783/c
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Shinn, P.

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Best Local
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Matches 53
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BH610787/c
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                  /clone="SAIK_04402"
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/clone=lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

129 c 86 g 115 t lothers
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
Alonso,J.M., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,F., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
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/db_xref="taxon:3702"
/dlone="SAIK_046918.54.75.x"
/clone="SAIK_A46918.54.75.x"
/clone="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
This sequence lies within an annotated exon of At1g16780.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

    .445
    /organism="Arabidopsis thaliana"
/strain="Columbia 0"

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/organism="Arabidopsis thaliana"
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                                     Location/Qualifiers
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                        tagged
                                                                                                                                                                                                                                                                                                                                                                                                 53; Conservative
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Matches
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                                     FEATURES
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BH610787 432 bp DNA linear GSS 04-JAN-2002 SALK_018043 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_018043, DNA sequence.
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bund at http://signal.salk.edu/tdna_protocols.html"
96 c 111 g 104 t
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arker, H., Prednis, L., Shinn, I
                                                                                                                                                                                                                                                                             329 CTCACIAIAGGGCACGCGTGGTCGACGGCCCGGGCTGCAGCTITGGGGGCGACGATCTCTG 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTTACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTATGAAGGTGGGAACCTCACTG 60
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Oppublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                     Length 440;
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                                                                                                                             Score 42.6; DB 17;
Pred. No. 0.057;
0; Mismatches 29;
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Location/Qualifiers
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                                                                                                                                4.18;
ilarity 67.48;
Conservative
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Arabidopsis thaliana
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Diffect Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 FVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecopl digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 129)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Klm,C.J., Parker,H., Prednis,L., Shinn,P.
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BH168812 GI:15904187
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                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : T7"
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/db_xref="taxon:3702"
/clone="sAkk 010562"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fraquent for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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A Sequence-Indexed Library of Insertion Mutations in the
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                              BH214178 500 bp DNA linear GSS 24-OCT-200 SALK_010362 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_010362, DNA sequence.
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BACR30M12 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL068402
GSS
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Contact: Joseph R. Ecker
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/strain=""Columbia 0" / db_xref="taxon:3702" / db_xref="taxon:3702" / clone="SALK_01803" / clone="SALK_01803" / clone="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 35 c 48 g 93 t
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/clone="SALK_008030"
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/clone="Lib="Axabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, eudioctyledons, core eudiocts,
Rosidae, eurosids_II; Brassicales, Brassicaceae; Arabidopsis.
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A Sequence-Indexed Library of Insertion Mutations in the
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llarity 73.0%; Pred. No. 0.067;
Conservative 0; Mismatches 20; Indels
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
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The Salk Institute For Biological Studies
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Fear: 858 6379
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/strain="Columbia 0"
             Location/Qualifiers
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/db xref="taxon:3702"
/clone="Statk_000216"
/clone="FCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

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Alonsoy.I.w., Leissey.T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C.J., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P. A Sequence-Indexed Library of Insertion Mutations in the
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  Zimmerman, J. and Ecker, J.R. Sequence-Indexed Library of Insertion Mutations in the
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Pred. No. 0.054;
0; Mismatches 35; Indels
                                                                                                                             Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 453 4100 x1752
Email: ecker@salk.edu
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
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/organism="Arabidopsis
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                                                     Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
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Zimmerman, J. and
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Best Local S:
Matches 63,
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Shinn, P.

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Local Similarity
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               61
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/strain="Columbia 0"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_047352.39.05.x"
/clone="SALK_047352.39.05.x"
/clone="Day as performed on Arabidopsis thaliana lines acch of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Rosidae; eurosids II: Brassicales; Brassicaceae, Arabidopsis.
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                                                                                                                             61 GATGCATATACTGCTGAGAGATAACATCACAATTCACAAGCTTCGATGTCACTACAGCCT 120
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                DB 17; Length 452;
                                                                     Indels
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Pred. No. 0.099;
0; Mismatches 12;
                                Score 42; DB 17; Le
Pred. No. 0.089;
0; Mismatches 55;
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80.3%;
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                                  4.1%;
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                                Query Match
Best Local Similarity 57.7
Matches 75; Conservative
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/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/clone_lib="Arabidopsis thaliana TDNA insertion lines fonce"EPER was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

100 c 101 g 124 t 3 others
   GSS 03-OCT-2001
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 457)
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A Sequence-Indexed Library of Insertion Mutations in the
BH172739 457 bp DNA linear GSS 03-OCT-20C SALK_006118 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_006118, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis Genome
Unpublished (2001)
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
Thoulo N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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pred. No. 0.12;
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/strain="Columbia 0"
/db_xref="taxon:3702"
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                                                                                                       BH172739.1 GI:15910808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ecker@salk.edu
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